STIC Search Report
Biotech-Chem Library

USPTO

STIC Database Tracking Number: 168123

TO: Elizabeth McElwain
Location: 2a11 / 2c18
Tuesday, October 11, 2005
Art Unit: 1638
Phone: 571-272-0802
Serial Number: 10 / 060793

From: Jan Delaval
Location: Biotech-Chem Library
Remsen 1a51
Phone: 571-272-2504

jan.delaval@uspto.gov

Search Notes

This Page Blank (uspto)

168123

From:	McElwain, Elizabeth
Sent:	Thursday, October 06, 2005 5:08 PM
To:	STIC-Biotech/ChemLib
Subject:	sequence search

Please search 10/060,793 for SEQ ID NO: 25 and for DNA encoding SEQ ID NO: 26.
Thank you,
Beth

Elizabeth F. McElwain, Ph.D.
U.S. Patent and Trademark Office
Tech Center 1600, Art Unit 1638
room Remsen 2A11
mailbox Remsen 2C18
571-272-0802
elizabeth.mcelwain@uspto.gov

RECEIVED
OCT -7 2005
TECH/CHEM. DIVISION
(STIC)

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

```
                    GenCore version 5.1.6

          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        October 11, 2005, 09:50:59 ; Search time 899 Seconds
                                           (without alignments)
                                    8343.865 Million cell updates/sec

Title:         US-10-060-793A-25
Perfect score: 1077
Sequence:      1 atgactgaggataagacgaa.........ccaaggccaagtcggactaa 1077

Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0

Searched:      8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters:        16885260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published Applications NA:*
          1:   /cgn2_6/ptcdata/2/pubpna/US07_PUBCOMB.seq:*
          2:   /cgn2_6/ptcdata/2/pubpna/PCT_NEW_PUB.seq:*
          3:   /cgn2_6/ptcdata/2/pubpna/US06_NEW_PUB.seq:*
          4:   /cgn2_6/ptcdata/2/pubpna/US06_PUBCOMB.seq:*
          5:   /cgn2_6/ptcdata/2/pubpna/US07_NEW_PUB.seq:*
          6:   /cgn2_6/ptcdata/2/pubpna/PCTUS_PUBCOMB.seq:*
          7:   /cgn2_6/ptcdata/2/pubpna/US08_NEW_PUB.seq:*
          8:   /cgn2_6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*
          9:   /cgn2_6/ptcdata/2/pubpna/US09A_PUBCOMB.seq:*
         10:   /cgn2_6/ptcdata/2/pubpna/US09B_PUBCOMB.seq:*
         11:   /cgn2_6/ptcdata/2/pubpna/US09C_PUBCOMB.seq:*
         12:   /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*
         13:   /cgn2_6/ptcdata/2/pubpna/US10A_PUBCOMB.seq:*
         14:   /cgn2_6/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*
         15:   /cgn2_6/ptcdata/2/pubpna/US10C_PUBCOMB.seq:*
         16:   /cgn2_6/ptcdata/2/pubpna/US10D_PUBCOMB.seq:*
         17:   /cgn2_6/ptcdata/2/pubpna/US10F_PUBCOMB.seq:*
         18:   /cgn2_6/ptcdata/2/pubpna/US10F_PUBCOMB.seq:*
         19:   /cgn2_6/ptcdata/2/pubpna/US10G_PUBCOMB.seq:*
         20:   /cgn2_6/ptcdata/2/pubpna/US10H_PUBCOMB.seq:*
         21:   /cgn2_6/ptcdata/2/pubpna/US10I_PUBCOMB.seq:*
         22:   /cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq:*
         23:   /cgn2_6/ptcdata/2/pubpna/US11A_PUBCOMB.seq:*
         24:   /cgn2_6/ptcdata/2/pubpna/US11_NEW_PUB.seq:*
         25:   /cgn2_6/ptcdata/2/pubpna/US60_NEW_PUB.seq:*
         26:   /cgn2_6/ptcdata/2/pubpna/US60_PUBCOMB.seq:*

                           SUMMARIES
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1077	100.0	1077	16	US-10-060-793-25	Sequence 25, Appl
2	1077	100.0	1077	19	US-10-776-311-41	Sequence 41, Appl
3	1077	100.0	1077	20	US-10-840-478-3	Sequence 3, Appli
4	1077	100.0	1077	21	US-10-840-325-35	Sequence 35, Appl
5	1077	100.0	1077	22	US-10-840-579-5	Sequence 5, Appli
c 6	1077	100.0	12456	22	US-10-985-109-95	Sequence 95, Appl
c 7	1077	100.0	12456	22	US-10-985-254-95	Sequence 95, Appl

```
 8  872.2  81.0  1077  20  US-10-840-478-62     Sequence 62, Appl
 9  872.2  81.0  1077  22  US-10-840-325-46     Sequence 46, Appl
10  872.2  81.0  1077  21  US-10-840-579-9      Sequence 9, Appli
11  869.6  80.7  10328 21  US-10-840-325-129    Sequence 129, App
12  869.6  80.7  10328 22  US-10-840-579-101    Sequence 101, App
13  158.6  14.7  1263  23  US-11-021-712-29     Sequence 29, Appl
14  113.2  10.5  1543  20  US-10-604-708-10     Sequence 10, Appl
15   113   10.5  1317  19  US-10-437-961-68012  Sequence 68012, A
16  111.2  10.3  1955  20  US-10-425-115-126240 Sequence 126240,
17  108.4  10.1  1553  20  US-10-425-115-81874  Sequence 81874, A
18  108.2  10.0  1766  20  US-10-739-930-2687   Sequence 2687, Ap
19    107   9.9  1182  16  US-10-060-793-41     Sequence 41, Appl
20  103.8   9.6  1976  19  US-10-437-961-25531  Sequence 25531, A
21  102.2   9.5  1242  20  US-10-491-733-7      Sequence 7, Appli
22  101.6   9.4  1797  18  US-10-425-114-19248  Sequence 19248, A
23  101.6   9.4  1804  20  US-10-425-115-73089  Sequence 73089, A
24  101.6   9.4  1804  20  US-10-604-708-9      Sequence 9, Appli
25  100.2   9.3  1829  20  US-10-425-115-73090  Sequence 73090, A
26    100   9.3  1733  15  US-10-223-646-2      Sequence 2, Appli
27   99.4   9.2  1666  20  US-10-425-115-126274 Sequence 126274,
28   97.6   9.1  1080  17  US-10-365-493-26432  Sequence 26432, A
29   97.6   9.1  2001  17  US-10-310-154-101    Sequence 101, App
30   97.6   9.1  2001  21  US-10-732-923-186    Sequence 186, App
31   96.6   9.0   103  20  US-10-840-478-76     Sequence 76, Appl
32   96.6   9.0   103  21  US-10-840-325-61     Sequence 61, Appl
33   96.6   9.0   103  22  US-10-840-579-23     Sequence 23, Appl
34   96.6   9.0   104  20  US-10-840-478-75     Sequence 75, Appl
35   96.6   9.0   104  21  US-10-840-325-60     Sequence 60, Appl
36   96.6   9.0   104  22  US-10-840-579-22     Sequence 22, Appl
37   95.4   8.9   757  19  US-10-767-701-4882   Sequence 4882, Ap
38   92.2   8.6   990  20  US-10-425-115-97175  Sequence 97175, A
39   91.6   8.5  1146  15  US-10-223-646-59     Sequence 59, Appl
40   91.6   8.5  1515  18  US-10-425-114-31496  Sequence 31496, A
41   91.6   8.5  1724  18  US-10-425-114-25066  Sequence 25066, A
42   91.6   8.5  1729  18  US-10-425-114-21414  Sequence 21414, A
43   91.6   8.5  1729  20  US-10-604-708-8      Sequence 8, Appli
44   91.6   8.5  1739  18  US-10-425-114-30705  Sequence 30705, A
45   91.6   8.5  1743  18  US-10-425-114-31268  Sequence 31268, A
```

```
                        ALIGNMENTS

RESULT 1
US-10-060-793-25
; Sequence 25, Application US/10060793
; Publication No.US20030196217A1
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT: Mukerji, Pradip
;  APPLICANT: Huang, Yung-Sheng
;  APPLICANT: Pereira, Suzette L.
;  TITLE OF INVENTION: DESATURASE GENES, ENZYMES ENCODED
;  TITLE OF INVENTION: THEREBY, AND USES THEREOF
;  FILE REFERENCE: 6884.US.O1
;  CURRENT APPLICATION NUMBER: US/10/060,793
;  CURRENT FILING DATE: 2002-06-24
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 25
;   LENGTH: 1077
;   TYPE: DNA
;   ORGANISM: Saprolegnia diclina
US-10-060-793-25

Query Match            100.0%;  Score 1077;  DB 16;  Length 1077;
Best Local Similarity  100.0%;  Pred. No. 4.2e-295;
Matches 1077;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCGACGCTCACGGAGCTCAAGCACTCGATC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCGACGCTCACGGAGCTCAAGCACTCGATC 60
```

GENERAL INFORMATION:
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Howard G. Damude
; APPLICANT: William D. Hitz
; APPLICANT: Anthony J. Kinney
; APPLICANT: Charles W. Kolar
; APPLICANT: Zhan Bin Liu
; TITLE OF INVENTION: Production of Long Chain Polyunsaturated Fatty Acids in Plants
; FILE REFERENCE: BB1538 US NA
; CURRENT APPLICATION NUMBER: US/10/776,311
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US 60/446,941
; PRIOR FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-776-311-41

Query Match   100.0%;   Score 1077;   DB 19;   Length 1077;
Best Local Similarity 100.0%; Pred. No. 4.2e-295;
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 ATGACTGAGGATAAGACGAAGCGTCGAGTTCCGACGCTCACGGAGCTCAAGCACTCGATC  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGACTGAGGATAAGACGAAGCGTCGAGTTCCGACGCTCACGGAGCTCAAGCACTCGATC  60

Qy  61 CCGAACGGCGTGCTTTGAGTCGAACCTCGGCCTCCTACTACACGGCCCGCGCCGGATC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 CCGAACGGCGTGCTTTGAGTCGAACCTCGGCCTCCTACTACACGGCCCGCGCCGGATC 120

Qy 121 TTCAACGCGTCGGCCTCGGCGGCGCTCGTCTCGACGGCCGTTCATTGCC 180
         |||||||||||||||||||||||||||||||||||||||||||
Db 121 TTCAACGCGTCGGCCTCGGCGGCGCTCGTCTCGACGGCCGTTCATTGCC 180

Qy 181 GATAACGTTCTGCTCACGCCGCCACTACATCTACGTGCAGGGCGTCATC 240
         |||||||||||||||||||||||||||||||||||||||||||||
Db 181 GATAACGTTCTGCTCACGCCGCCACTACATCTACGTGCAGGGCGTCATC 240

Qy 241 TTCTGGGCCTTCTCACGGTCGGCCACGACTGCGGCCTTCTCGCGCTACCAC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TTCTGGGCCTTCTCACGGTCGGCCACGACTGCGGCCTTCTCGCGCTACCAC 300

Qy 301 AGCGTCAACTTTATCATCGGCTGCATCATGCATCATCGGCTTTGCGTCATG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AGCGTCAACTTTATCATCGGCTGCATCATGCATCATCGGCTTTGCGTCATG 360

Qy 361 TGGCGGCGTGACGACCGCCACCGGTCGGTCAAGGACCTTCAGGAACACAGGAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 TGGCGGCGTGACGACCGCCACCGGTCGGTCAAGGACCTTCAGGAACACAGGAC 420

Qy 421 TTTTACCCGACCACGGTCGGTCAAGGACCTTCCAATGGGTCTACACGCTC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TTTTACCCGACCACGGTCGGTCAAGGACCTTCCAATGGGTCTACACGCTC 480

Qy 481 GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCGACGATGAGC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCGACGATGAGC 540

Qy 541 GACCCGTGGGACCCGCCTTCTTCGCGCCGGTCATCGTGTCGCTCGGCGTC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GACCCGTGGGACCCGCCTTCTTCGCGCCGGTCATCGTGTCGCTCGGCGTC 600

Qy 601 TGGGCCGCCCTTCTTCGCCGCCGGTACGGCCGTACTCGGCTTTGCGTCATG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TGGGCCGCCCTTCTTCGCCGCCGGTACGGCCGTACTCGGCTTTGCGTCATG 660
```

```
Qy  61 CCGAACGCGTCGGCCTCGGCCGCGCTGCTTCGGGCGCGCTCCTTCGCCTCCTCGCTTCATTGCC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 CCGAACGCGTCGGCCTCGGCCGCGCTGCTTCGGGCGCGCTCCTTCGCCTCCTCGCTTCATTGCC 120

Qy 121 TTCAACGCGTCGGCCTCGGCGGCGCTCGTCTCGACGGCCGTTCATTGCC 180
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TTCAACGCGTCGGCCTCGGCGGCGCTCGTCTCGACGGCCGTTCATTGCC 180

Qy 181 GATAACGTTCTGCTCACGCCGCCACTACATCTACGTGCAGGGCGTCAGC 240
         |||||||||||||||||||||||||||||||||||||||||||
Db 181 GATAACGTTCTGCTCACGCCGCCACTACATCTACGTGCAGGGCGTCAGC 240

Qy 241 TTCTGGGCCTTCTCACGGTCGGCCACGACTGCGGCCTTCTCGCGCTACCAC 300
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TTCTGGGCCTTCTCACGGTCGGCCACGACTGCGGCCTTCTCGCGCTACCAC 300

Qy 301 AGCGTCAACTTTATCATCGGCTGCATCATGCATCATCGGCTTTGCGTCATG 360
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AGCGTCAACTTTATCATCGGCTGCATCATGCATCATCGGCTTTGCGTCATG 360

Qy 361 TGGCGGCGTGACGACCGCCACCGGTCGGTCAAGGACCTTCAGGAACGACGAGAGC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 TGGCGGCGTGACGACCGCCACCGGTCGGTCAAGGACCTTCAGGAACGACGAGAGC 420

Qy 421 TTTTACCCGACCACGGTCGGTCAAGGACCTTCCAATGGGTCTACACGCTC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TTTTACCCGACCACGGTCGGTCAAGGACCTTCCAATGGGTCTACACGCTC 480

Qy 481 GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCGACCGCCACCAC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCGACCGCCACCAC 540

Qy 541 GACCCGTGGGACCCGTGGGACCCGCCCTCTTTCGCGCCGGTCATCGTGTCGCTCGGCGTC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GACCCGTGGGACCCGTGGGACCCGCCCTCTTTCGCGCCGGTCATCGTGTCGCTCGGCGTC 600

Qy 601 TGGGCCGCCCTTCTTCGCCGCCGGTACGGCCGTACTCGGCTTTGCGTCATG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TGGGCCGCCCTTCTTCGCCGCCGGTACGGCCGTACTCGGCTTTGCGTCATG 660

Qy 661 GGCCTCTACTACTACTTGTCTTTGCTTTGCTTTCGTTCCTCGTCATTACGACCTTC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 GGCCTCTACTACTACTTGTCTTTGCTTTGCTTTCGTTCCTCGTCATTACGACCTTC 720

Qy 721 TTGCACCACAACGACGACGAAGCGACGCCGTGGTACGGCGCGTCGACGCCGTCGACAACCTGAGCCACCAC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 TTGCACCACAACGACGACGAAGCGACGCCGTGGTACGGCGCGTCGACGCCGTCGACAACCTGAGCCACCAC 780

Qy 781 GGCAACCTTCGAGCGCTCGACGCCGTTGGACGTGGACAACCTGAGCCACCAC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 GGCAACCTTCGAGCGCTCGACGCCGTTGGACGTGGACAACCTGAGCCACCAC 840

Qy 841 ATTGGCACGACCAGTCCACCACTTGTCTCCCGATCATTCCGCACTACAAGCTCAAGCGAA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 ATTGGCACGACCAGTCCACCACTTGTCTCCCGATCATTCCGCACTACAAGCTCAAGCGAA 900

Qy 901 GCCACCAAGCACTTTGCGCGGCGTACCCGCGCACTCGTGCGGAACGACGAGCGCCATC 960
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 GCCACCAAGCACTTTGCGCGGCGTACCCGCGCACTCGTGCGGAACGACGAGCGCCATC 960

Qy 961 ATCACGCGCCTTCTTCAAGACCCGCCACACCTCTTTGTCAACTACACGGCCCGTGCCCGAGACG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 ATCACGCGCCTTCTTCAAGACCCGCCACACCTCTTTGTCAACTACACGGCCCGTGCCCGAGACG 1020

Qy 1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCCCGCCAAGGCCAAGTCGGACTAA 1077
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCCCGCCAAGGCCAAGTCGGACTAA 1077
```

RESULT 2
US-10-776-311-41
; Sequence 41, Application US/10776311
; Publication No. US20040172682A1

```
Qy   721 TTGCACCACCACGACGAAGCGACGCCGTGGTACGGCGACTCGGAGTGGACGTACGTCAAG 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TTGCACCACCACGACGAAGCGACGCCGTGGTACGGCGACTCGGAGTGGACGTACGTCAAG 780

Qy   781 GGCAACCTCTCGAGCGTCGACCGGTCGACGCGCGCGTCGTGTGACAACCTGAGCCACCAC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCAACCTCTCGAGCGTCGACCGGTCGACGCGCGCGTCGTGTGACAACCTGAGCCACCAC 840

Qy   841 ATTGGCACGACCAGGTCCACCACTTGTTCCGATCATTCCCGACTACAAGCTCAACGAA 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATTGGCACGACCAGGTCCACCACTTGTTCCGATCATTCCCGACTACAAGCTCAACGAA 900

Qy   901 GCCACCAAGCACTTTGCGGCCCGCGTACCCGCACCTCGTGCCCGCAGGAACGACGAGCCCATC 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCCACCAAGCACTTTGCGGCCCGCGTACCCGCACCTCGTGCCCGCAGGAACGACGAGCCCATC 960

Qy   961 ATCACGGCCTTCTTCAAGACCTCGTGTGCCCGTGCCCGAGACG 1020
         |||||||||||||||||||||||||||||||||||||||||||
Db   961 ATCACGGCCTTCTTCAAGACCTCGTGTGCCCGTGCCCGAGACG 1020

Qy  1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCGCCGGCCCAAGGCCAAGTCGGACTAA 1077
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCGCCGGCCCAAGGCCAAGTCGGACTAA 1077
```

RESULT 3
US-10-840-478-3
; Sequence 3, Application US/10840478
; Publication No. US20040253621A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: OPTIMIZED GENES FOR THE PRODUCTION OF OMEGA FATTY ACIDS IN
; TITLE OF INVENTION: OLEAGINOUS YEASTS
; FILE REFERENCE: CL2234 US NA
; CURRENT APPLICATION NUMBER: US/10/840,478
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US60/468718
; PRIOR FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US60/468677
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina (ATCC #56851)
US-10-840-478-3

```
Query Match     100.0%;    Score 1077;   DB 20;   Length 1077;
Best Local Similarity  100.0%;   Pred. No. 4.2e-295;
Matches 1077;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1 ATGACTGAGGATAAGACGAAGTCGAGTTCCGACGCTCACGGAGCTCAAGCACTCGATC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGACTGAGGATAAGACGAAGTCGAGTTCCGACGCTCACGGAGCTCAAGCACTCGATC 60

Qy    61 CCGAACCGGTGCTTTGAGTCGAACCTCGGCCTTCGCGGCCTCGCTCGCTACACGCCGCGGATC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCGAACCGGTGCTTTGAGTCGAACCTCGGCCTTCGCGGCCTCGCTCGCTACACGCCGCGGATC 120

Qy   121 TTCAACGGCGTCGGCCTCGGCCTGTCTCACGCGGCGCGCTCGAGCGCCGTTCATTGCC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTCAACGGCGTCGGCCTCGGCCTGTCTCACGCGGCGCGCTCGAGCGCCGTTCATTGCC 180

Qy   181 GATAACGTTCTGCTCCACGCGCGCGTTGCGCCACCTACGTGCAGGGCGTCATC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATAACGTTCTGCTCCACGCGCGCGTTGCGCCACCTACGTGCAGGGCGTCATC 240

Qy   241 TTCTGGGGCTTCTTCACGGTCCGGCCACGACTGCGGCCACTACGCCTTCTCCGCGTACCAC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTCTGGGGCTTCTTCACGGTCCGGCCACGACTGCGGCCACTACGCCTTCTCCGCGTACCAC 300
```

```
Qy   301 AGGGTCAACTTTATCATCGGCTGCATCATGACCATCTGCGGATTTTGACGCCGTTCGAGAGC 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGGGTCAACTTTATCATCGGCTGCATCATGACCATCTGCGGATTTTGACGCCGTTCGAGAGC 360

Qy   361 TGGCGGTGAGCACCGGCCACCACCACCAGACACGGGCAACATTGATAAGGACGAGATC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TGGCGGTGAGCACCGGCCACCACCACCAGACACGGGCAACATTGATAAGGACGAGATC 420

Qy   421 TTTTACCGCACCGGTCGGTCAAGGACCTCCAGGACGTCGCGCCAATGGTCTACACGCTC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTTACCGCACCGGTCGGTCAAGGACCTCCAGGACGTCGCGCCAATGGTCTACACGCTC 480

Qy   481 GGCGGTGGCTGGTTGTCTACTTGAAGGTCGGGTATGCCCGCGCACGATGAGCCACTTT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGCGGTGGCTGGTTGTCTACTTGAAGGTCGGGTATGCCCGCGCACGATGAGCCACTTT 540

Qy   541 GACCGTGGGACCCGGCTCTTCCTTCGCGGCGTCATCGTGTCGCTCGGCGTC 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GACCGTGGGACCCGGCTCTTCCTTCGCGGCGTCATCGTGTCGCTCGGCGTC 600

Qy   601 TGGCCGGCCTTCTTCGGCCGTACGGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGGCCGGCCTTCTTCGGCCGTACGGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG 660

Qy   661 GGCCTCTACTACTATGCGCCGCCTCTTCTTGCTTCGTCTCTTCGTTCCTCGTCATTACGACCTTC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGCCTCTACTACTATGCGCCGCCTCTTCTTGCTTCGTCTCTTCGTTCCTCGTCATTACGACCTTC 720

Qy   721 TTGCACCACCACGACGAAGCGACCGTGGTACGGCGACTCGGAGTGGACGTACGTCAAG 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TTGCACCACCACGACGAAGCGACCGTGGTACGGCGACTCGGAGTGGACGTACGTCAAG 780

Qy   781 GGCAACCTCTCGAGCGTCGACCGGTCGACCGGTCGTGTGACAACCTGAGCCACCAC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCAACCTCTCGAGCGTCGACCGGTCGACCGGTCGTGTGACAACCTGAGCCACCAC 840

Qy   841 ATTGGCACGACCAGGTCCACCACTTGTTCCGATCATTCCCGATCATTCCCGACTACAAGCTCAACGAA 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATTGGCACGACCAGGTCCACCACTTGTTCCGATCATTCCCGATCATTCCCGACTACAAGCTCAACGAA 900

Qy   901 GCCACCAAGCACTTTGCGGCCCGCGTACCCGCACCTCGTGCCGCAGGAACGACGAGCCCATC 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCCACCAAGCACTTTGCGGCCCGCGTACCCGCACCTCGTGCCGCAGGAACGACGAGCCCATC 960

Qy   961 ATCACGGCCTTCTTCAAGACCTCTTGTTCAACTACGGCGCCCACTCCTTGTCAACTACGGCGCCCAGACG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATCACGGCCTTCTTCAAGACCTCTTGTTCAACTACGGCGCCCACTCCTTGTCAACTACGGCGCCCAGACG 1020

Qy  1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCGCCGGCCCGCCCAAGGCCAAGTCGGACTAA 1077
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCGCCGGCCCGCCCAAGGCCAAGTCGGACTAA 1077
```

RESULT 4
US-10-840-325-35
; Sequence 35, Application US/10840325
; Publication No. US20050043527A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; TITLE OF INVENTION: A DELTA-12 DESATURASE GENE SUITABLE FOR ALTERING LEVELS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN OLEAGINOUS YEASTS
; FILE REFERENCE: CL2301
; CURRENT APPLICATION NUMBER: US/10/840,325
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US 60/484209
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US 60/468677
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35

```
;  LENGTH: 1077
;  TYPE: DNA
;  ORGANISM: Saprolegnia diclina
US-10-840-325-35

Query Match       100.0%;   Score 1077;  DB 21; Length 1077;
Best Local Similarity  100.0%;  Pred. No. 4.2e-295;
Matches 1077;   Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  ATGACTGAGGATAAGACGAAGTCGAGTTCCGACCGCTCACGGAGCTCAAGCACTCGATC   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATGACTGAGGATAAGACGAAGTCGAGTTCCGACCGCTCACGGAGCTCAAGCACTCGATC   60

Qy   61  CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCCTCTACACGGCCCGCGCGATC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCCTCTACACGGCCCGCGCGATC  120

Qy  121  TTCAACGCGTCGGCCTCGGCCGCTGCTCTACGGCGGCGGCCGTTCATTGCC          180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  TTCAACGCGTCGGCCTCGGCCGCTGCTCTACGGCGGCGGCCGTTCATTGCC          180

Qy  181  GATAACGTTCTGCTCCACGCTGCGGCCACCTACGTGCAGGGCGTCATC              240
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  GATAACGTTCTGCTCCACGCTGCGGCCACCTACGTGCAGGGCGTCATC              240

Qy  241  TTCTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTCGGCCTTCTCGCGTACCAC   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  TTCTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTCGGCCTTCTCGCGTACCAC   300

Qy  301  AGCGTCAACTTTATCATCGGCTGCATCATGCGACTCTGCGATTTTGACGCCGTTCGAGAGC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  AGCGTCAACTTTATCATCGGCTGCATCATGCGACTCTGCGATTTTGACGCCGTTCGAGAGC 360

Qy  361  TGGCGCGGTGACGCACCGCCACCACCAAGAACACGGCAACATTGATAAGGACGAGATC    420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  TGGCGCGGTGACGCACCGCCACCACCAAGAACACGGCAACATTGATAAGGACGAGATC    420

Qy  421  TTTTACCCGACCGGTCGGTCAAGGACCTCCAGGAGTGCGCCAATGGGTCTACACGCTC    480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  TTTTACCCGACCGGTCGGTCAAGGACCTCCAGGAGTGCGCCAATGGGTCTACACGCTC    480

Qy  481  GGCGGGTGCGTGGTTGTCTACTTGAAGGTCGGGTATGCCCCGCGACGATGAGCCACTTT   540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GGCGGGTGCGTGGTTGTCTACTTGAAGGTCGGGTATGCCCCGCGACGATGAGCCACTTT   540

Qy  541  GACCCGTGGGACCGCCTCTTCGCGCGGTACCGTGTCATCGTGTCCGCTTTGCCGTCATG   600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GACCCGTGGGACCGCCTCTTCGCGCGGTACCGTGTCATCGTGTCCGCTTTGCCGTCATG   600

Qy  601  TGGGCGCCTTCTTCGCGCGGTACCTCACATACTCGCTTCCTCGTCATTACGACCTTC    660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  TGGGCGCCTTCTTCGCGCGGTACCTCACATACTCGCTTCCTCGTCATTACGACCTTC    660

Qy  661  GGCCTCACTACTATCGCGCCGCCTCTTTGTCTTGCTTCGTTGCTCGTCATTACGGCCTTC  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  GGCCTCACTACTATCGCGCCGCCTCTTTGTCTTGCTTCGTTGCTCGTCATTACGGCCTTC  720

Qy  721  TTGCACCACAACGACGAAGGCACGACGGCCCGTGGTACGGCGACTCGGAGTCAGTCAAG   780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  TTGCACCACAACGACGAAGGCACGACGGCCCGTGGTACGGCGACTCGGAGTCAGTCAAG   780

Qy  781  GGCAACCTCTGAGCCGTCGACCGCGTTCGTCGGTGGACAACCTGAGCCACCAC        840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  GGCAACCTCTGAGCCGTCGACCGCGTTCGTCGGTGGACAACCTGAGCCACCAC        840

Qy  841  ATTGGCACGACCAGGTCCACCACTTGTCCCGGCCACTTGTTCCGCCACTACAAGCTCAACGAA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  ATTGGCACGACCAGGTCCACCACTTGTCCCGGCCACTTGTTCCGCCACTACAAGCTCAACGAA 900

Qy  901  GCCACCAAGCACTTTGGGGCCCGCTACCGGCGCACCCGGCCACCC              960
         |||||||||||||||||||||||||||||||||||||||||||||
Db  901  GCCACCAAGCACTTTGGGGCCCGCTACCGGCGCACCCGGCCACCC              960
```

RESULT 5
US-10-840-579-5

```
;  Sequence 5, Application US/10840579
;  Publication No. US20050136519A1
;  GENERAL INFORMATION:
;  APPLICANT: E.I. du Pont de Nemours and Company, Inc.
;  TITLE OF INVENTION: PRODUCTION OF OMEGA FATTY ACIDS IN OLEAGINOUS YEASTS
;  FILE REFERENCE: CL2233 PCT
;  CURRENT APPLICATION NUMBER: US/10/840,579
;  CURRENT FILING DATE: 2004-05-06
;  PRIOR APPLICATION NUMBER: US 60/468677
;  PRIOR FILING DATE: 2003-05-07
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 5
;  LENGTH: 1077
;  TYPE: DNA
;  ORGANISM: Saprolegnia diclina (ATCC #56851)
US-10-840-579-5

Query Match       100.0%;   Score 1077;  DB 22; Length 1077;
Best Local Similarity  100.0%;  Pred. No. 4.2e-295;
Matches 1077;   Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  ATGACTGAGGATAAGACGAAGTCGAGTTCCGACCGCTCACGGAGCTCAAGCACTCGATC   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATGACTGAGGATAAGACGAAGTCGAGTTCCGACCGCTCACGGAGCTCAAGCACTCGATC   60

Qy   61  CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCCTCTACACGGCCCGCGCGATC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCCTCTACACGGCCCGCGCGATC  120

Qy  121  TTCAACGCGTCGGCCTCGGCCGCGTGCTCTACGGCGGCGGCCGTTCATTGCC         180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  TTCAACGCGTCGGCCTCGGCCGCGTGCTCTACGGCGGCGGCCGTTCATTGCC         180

Qy  181  GATAACGTTCTGCTCCACGCTGCGGCCACCTACGTGCAGGGCGTCATC              240
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  GATAACGTTCTGCTCCACGCTGCGGCCACCTACGTGCAGGGCGTCATC              240

Qy  241  TTCTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTCGGCCTTCTCGCGTCGGCGTC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  TTCTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTCGGCCTTCTCGCGTCGGCGTC 300

Qy  301  AGCGTCAACTTTATCATCGGCTGCATCATGCGACTCTGCGATTTTGACGCCGTTCGAGAGC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  AGCGTCAACTTTATCATCGGCTGCATCATGCGACTCTGCGATTTTGACGCCGTTCGAGAGC 360

Qy  361  TGGCGCGGTGACGCACCGCCACCACCAAGAACACGGCAACATTGATAAGGACGAGATC    420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  TGGCGCGGTGACGCACCGCCACCACCAAGAACACGGCAACATTGATAAGGACGAGATC    420

Qy  421  CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCCTCTACACGGCCCGCGCGATC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCCTCTACACGGCCCGCGCGATC  480

Qy  481  TTCAACGCGTCGGCCTCGGCCGCGTGCTCTACGGCGGCGGCCGTTCATTGCC         540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  TTCAACGCGTCGGCCTCGGCCGCGTGCTCTACGGCGGCGGCCGTTCATTGCC         540

Qy  541  GACCCGTGGGACCGCGTGGTTGTTTGCTACTTGCTACTTGAAGGTCGGTATGCCGCGTC   600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GACCCGTGGGACCGCGTGGTTGTTTGCTACTTGCTACTTGAAGGTCGGTATGCCGCGTC   600

Qy  961  ATCACGGCCTTCTTCAAGACCCGCCACCTCTTTGTCAACTACGGCGGCTGTGCCCGAGACG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  ATCACGGCCTTCTTCAAGACCCGCCACCTCTTTGTCAACTACGGCGGCTGTGCCCGAGACG 1020

Qy 1021  GCGCAGATCTTCACGCTCAAAGAGTCGGCCCGGCCCCAAGGCCCAAGTCGGACTAA      1077
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  GCGCAGATCTTCACGCTCAAAGAGTCGGCCCGGCCCCAAGGCCCAAGTCGGACTAA      1077
```

```
Qy    601 TGGGCCGCTTCTTCGCGCGTACGGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGGGCCGCTTCTTCGCGCGTACGGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG 660

Qy    661 GGCCTCTACTACTATGCGCGCTCTTCGTTCCTCGTTCGTTCCTCGTCATTACGACCTTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGCCTCTACTACTATGCGCGCTCTTCGTTCCTCGTTCGTTCCTCGTCATTACGACCTTC 720

Qy    721 TTGCACCACAACGACGAAGGCGACGCCGTGGTACGGCGCACTCGGAGTGACGTACGTCAAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTGCACCACAACGACGAAGGCGACGCCGTGGTACGGCGCACTCGGAGTGACGTACGTCAAG 780

Qy    781 GGCAACCTCTCGACGCGTCGTACGGCGCGTTCGTGGACAACCTGAGCCACCAC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCAACCTCTCGACGCGTCGTACGGCGCGTTCGTGGACAACCTGAGCCACCAC 840

Qy    841 ATTGGCACGCACCAGGTCCACCACTTGTTCCCGATCATTCCCGACTACAAGCTCAACGAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATTGGCACGCACCAGGTCCACCACTTGTTCCCGATCATTCCCGACTACAAGCTCAACGAA 900

Qy    901 GCCACCAAGCACTTTGCGCGCCGCGTACCCGCCGTACCGCGCACCTCTTGTGCGAGGAACGACGAGCCCATC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCACCAAGCACTTTGCGCGCCGCGTACCCGCCGTACCGCGCACCTCTTGTGCGAGGAACGACGAGCCCATC 960

Qy    961 ATCACGGCCTTCTTCAAGACCTCGTGCCGCACCTCTTTGTCAACTACGGCGTGTGCCCGAGACG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATCACGGCCTTCTTCAAGACCTCGTGCCGCACCTCTTTGTCAACTACGGCGTGTGCCCGAGACG 1020

Qy   1021 GGGCAGATCTTCACGCTCAAAGAGTCGGCCGCGCCAAGGCCAAGTCGGACTAA 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGGCAGATCTTCACGCTCAAAGAGTCGGCCGCGCCAAGGCCAAGTCGGACTAA 1077
```

RESULT 6
US-10-985-109-95/c
; Sequence 95, Application US/10985109
; Publication No. US2005013244lAl
; GENERAL INFORMATION:
; APPLICANT: Yadav, Narendra
; APPLICANT: Damude, Howard
; TITLE OF INVENTION: DELTA-15 DESATURASES SUITABLE FOR ALTERING LEVELS OF POLYUNSATURA
; TITLE OF INVENTION: FATTY ACIDS IN OILSEED PLANTS AND OLEAGINOUS YEAST
; FILE REFERENCE: CL2432
; CURRENT APPLICATION NUMBER: US/10/985,109
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/519191
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 95
; LENGTH: 12456
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid pKR585
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1201)..(1201)
; OTHER INFORMATION: n is a, c, g, or t
US-10-985-109-95

Query Match   100.0%; Score 1077; DB 22; Length 12456;
Best Local Similarity 100.0%; Pred. No. 6.8e-295;
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGACGCTCACGCAGCTCAAGCACTCGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10446 ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGACGCTCACGCAGCTCAAGCACTCGATC 10387

Qy     61 CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGGCCCTCGCGCTCTTCGCGCTACTACACGGCCCCGCCGGATC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10386 CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGGCCCTCGCGCTCTTCGCGCTACTACACGGCCCCGCCGGATC 10327
```

```
Qy    121 TTCAACGGGTCGGCCTCGGCCTCGGCGGCGGCGGCGCTCGACCGCCGTCATTGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10326 TTCAACGGGTCGGCCTCGGCCTCGGCGGCGGCGGCGCTCGACCGCCGTCATTGCC 10267

Qy    181 GATAACGTTCTGCTCCACGCGTCGTTGCGCCACCTACATCACGTGCAGGGCGTCATC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10266 GATAACGTTCTGCTCCACGCGTCGTTGCGCCACCTACATCACGTGCAGGGCGTCATC 10207

Qy    241 TTCTGGGCTTCTTCACGGTCGGCCACGACTCGGCCTTCGCGGCCTTCGCGCCTACCAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10206 TTCTGGGCTTCTTCACGGTCGGCCACGACTCGGCCTTCGCGGCCTTCGCGCCTACCAC 10147

Qy    301 AGGGTCAACTTATCATCGGCTGCATCATGCACTCTGCGATTTTGACCCGGTCGAGAGC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10146 AGGGTCAACTTATCATCGGCTGCATCATGCACTCTGCGATTTTGACCCGGTCGAGAGC 10087

Qy    361 TGGCGCGTGACGGCACCGCACCACCAAGAACACGGCAACATTGATAAGGACGAGATC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10086 TGGCGCGTGACGGCACCGCACCACCAAGAACACGGCAACATTGATAAGGACGAGATC 10027

Qy    421 TTTTACCCGCCACCGGTCGGTCAAGGACGTGCGCCAATGGGTCTACACGCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10026 TTTTACCCGCCACCGGTCGGTCAAGGACGTGCGCCAATGGGTCTACACGCTC 9967

Qy    481 GGCGGTGCGTGGTTTGTCACTTGAAGGTCGGGTATGCCCGCGCACGAGGTCGGCGCACTTT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9966 GGCGGTGCGTGGTTTGTCACTTGAAGGTCGGGTATGCCCGCGCACGAGGTCGGCGCACTTT 9907

Qy    541 GACCCGTGGGACCCGCTCCTCTTCGCGCGTACGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9906 GACCCGTGGGACCCGCTCCTCTTCGCGCGTACGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG 9847

Qy    601 TGGGCCGCTTCTTCGCGCGTACGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9846 TGGGCCGCTTCTTCGCGCGTACGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG 9787

Qy    661 GGCCTCTACTACTATGCGCGCTCTTCGTTCCTCGTTCGTTCCTCGTCATTACGACCTTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9786 GGCCTCTACTACTATGCGCGCTCTTCGTTCCTCGTTCGTTCCTCGTCATTACGACCTTC 9727

Qy    721 TTGCACCACAACGACGAAGGCGACGCCGTGGTACGGCGCACTCGGAGTGACGTACGTCAAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9726 TTGCACCACAACGACGAAGGCGACGCCGTGGTACGGCGCACTCGGAGTGACGTACGTCAAG 9667

Qy    781 GGCAACCTCTCGAGCGTCGTGTGGACAACCTGAGCCACCAC 840
          |||||||||||||||||||||||||||||||||||||||||
Db   9666 GGCAACCTCTCGAGCGTCGTGTGGACAACCTGAGCCACCAC 9607

Qy    841 ATTGGCACGCACCAGGTCCACCACTTGTTCCCGATCATTCCGATCATTCCGACTACAAGCTCAACGAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9606 ATTGGCACGCACCAGGTCCACCACTTGTTCCCGATCATTCCGATCATTCCGACTACAAGCTCAACGAA 9547

Qy    901 GCCACCAAGCACTTGGGCGTACCCGGCGTACCCGCGCACCTCGTGCGCAGGAACGACGAGCCCATC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9546 GCCACCAAGCACTTGGGCGTACCCGGCGTACCCGCGCACCTCGTGCGCAGGAACGACGAGCCCATC 9487

Qy    961 ATCACGGCCTTCTTCAAGACCTCTTTGTCAACTACACGGCGCGTGTGCCCCGAGACG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9486 ATCACGGCCTTCTTCAAGACCTCTTTGTCAACTACACGGCGCGTGTGCCCCGAGACG 9427

Qy   1021 GGGCAGATCTTCACGCTCAAAGAGTCGGCCGCGCCAAGGCCAAGTCGGACTAA 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9426 GGGCAGATCTTCACGCTCAAAGAGTCGGCCGCGCCAAGGCCAAGTCGGACTAA 9370
```

RESULT 7
US-10-985-254-95/c
; Sequence 95, Application US/10985254
; Publication No. US2005013442A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Co., Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Damude, Howard

```
; TITLE OF INVENTION: DELTA 15 DESATURASES SUITABLE FOR ALTERING LEVELS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN OLEAGINOUS YEAST
; FILE REFERENCE: CL2432
; CURRENT APPLICATION NUMBER: US/10/985,254
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/519191
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 12456
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid pKR585
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1201)..(1201)
; OTHER INFORMATION: n is a, c, g, or t
US-10-985-254-95

Query Match         100.0%;  Score 1077;  DB 22;  Length 12456;
Best Local Similarity 100.0%;  Pred. No. 6.8e-295;
Matches 1077;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ATGACTGAGGATAAGACGAAGGTCGAAGGTCGAGTTCCCGACGCTCACGGAGCTCAAGCACTCGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10446 ATGACTGAGGATAAGACGAAGGTCGAAGGTCGAGTTCCCGACGCTCACGGAGCTCAAGCACTCGATC 10387

Qy     61 CCGAACGCGGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCTACTACACGGCCCGGCGGATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10386 CCGAACGCGGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCTACTACACGGCCCGGCGGATC 10327

Qy    121 TTCAACGCGTCGGCCTCGGCCTGCTCTACGGCGGCGCTCGACGCCCGTTCATTGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10326 TTCAACGCGTCGGCCTCGGCCTGCTCTACGGCGGCGCTCGACGCCCGTTCATTGCC 10267

Qy    181 GATAACGTTCTGCTCCACGCGCTCGTTTGCGCACTACGTGCAGGGCGTCATC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10266 GATAACGTTCTGCTCCACGCGCTCGTTTGCGCACTACGTGCAGGGCGTCATC 10207

Qy    241 TTCTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTTCTCGCGCTACCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10206 TTCTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTTCTCGCGCTACCAC 10147

Qy    301 AGCGTCAACTTTATCATCGGCTGCATCATGGCAACATTGATAAGGACAGGATC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10146 AGCGTCAACTTTATCATCGGCTGCATCATGGCAACATTGATAAGGACAGGATC 10087

Qy    361 TGGCCGGTGACGACCACCGGTCGGTCAAGGACCTCCAGGACGTGCGCCAATGGGTCTACACGCTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10086 TGGCCGGTGACGACCACCGGTCGGTCAAGGACCTCCAGGACGTGCGCCAATGGGTCTACACGCTC 10027

Qy    421 TTTTACCCGACACCGGTCGGTCAAGGACCTCCAGGACGTCGCCAATGGGTCTACACGCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10026 TTTTACCCGACACCGGTCGGTCAAGGACCTCCAGGACGTCGCCAATGGGTCTACACGCTC 9967

Qy    481 GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCACGATGAGCCACTTT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9966 GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCACGATGAGCCACTTT 9907

Qy    541 GACCCGTGGGACCCCGCTCCTCCTTGCGCCGCCGTCATCGTGTCGTCGGCGTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9906 GACCCGTGGGACCCCGCTCCTCCTTGCGCCGCCGTCATCGTGTCGTCGGCGTC 9847

Qy    601 TGGGGCCGCCTTCTTCGGCCGGCTACCTCACGCTACCTCACATACTCGCTCGGCTTTGCCTTGCATG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9846 TGGGGCCGCCTTCTTCGGCCGGCTACCTCACGCTACCTCACATACTCGCTCGGCTTTGCCTTGCATG 9787

Qy    661 GGCCTCTACTACTATGCGCGCCCTCTTTGTTCGTTCGTTGCTTCGTCGTTCCTCGTTCATTACGACCTTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9786 GGCCTCTACTACTATGCGCGCCCTCTTTGTTCGTTCGTTGCTTCGTCGTTCCTCGTTCATTACGACCTTC 9727
```

```
Qy    721 TTGCACCACCAACGACGAGCGACGCGCCCTGGTACGGCGACTCGGAGTGGACGTACGTCAAG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9726 TTGCACCACCAACGACGAGCGACGCGCCCTGGTACGGCGACTCGGAGTGGACGTACGTCAAG 9667

Qy    781 GGCAACCTCTCGAGCGTCGACCGGCGTCGACCGGCGCGCGTTCGTTGGACAACCTGGACAACCTGACGCCACCAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9666 GGCAACCTCTCGAGCGTCGACCGGCGTCGACCGGCGCGCGTTCGTTGGACAACCTGGACAACCTGACGCCACCAC 9607

Qy    841 ATTGGCACGCACCAGGTCCACCACTTGTTCCCGATCATTCCGCCACTACAAGCTCAACGAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9606 ATTGGCACGCACCAGGTCCACCACTTGTTCCCGATCATTCCGCCACTACAAGCTCAACGAA 9547

Qy    901 GCCACCAAGCACTTTGCGGCCCGTACCCGTACCCGTCGTGCGCCAGGACGACGAGCCCATC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9546 GCCACCAAGCACTTTGCGGCCCGTACCCGTACCCGTCGTGCGCCAGGACGACGAGCCCATC 9487

Qy    961 ATCACGGCCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGGCCGTGTGCCCGAGACG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9486 ATCACGGCCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGGCCGTGTGCCCGAGACG 9427

Qy   1021 GCGCGAGATCTTCACGCTCAAAGAGTCGGCCCGGCGCCCAAGGCCAAGTCGGACTAA 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9426 GCGCGAGATCTTCACGCTCAAAGAGTCGGCCCGGCGCCCAAGGCCAAGTCGGACTAA 9370
```

```
RESULT 8
US-10-840-478-62
; Sequence 62, Application US/10840478
; Publication No. US20040253621A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.
; APPLICANT: Zhu, Quinn
; APPLICANT: Picataggio, Stephen K.
; TITLE OF INVENTION: OPTIMIZED GENES FOR THE PRODUCTION OF OMEGA FATTY ACIDS IN
; TITLE OF INVENTION: OLEAGINOUS YEASTS
; FILE REFERENCE: CL2234 US NA
; CURRENT APPLICATION NUMBER: US/10/840,478
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US60/468718
; PRIOR FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US60/468677
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-840-478-62

Query Match          81.0%;  Score 872.2;  DB 20;  Length 1077;
Best Local Similarity 88.1%;  Pred. No. 5.1e-237;
Matches 949;  Conservative 0;  Mismatches 128;  Indels 0;  Gaps 0;

Qy      1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGACGCTCACGGAGCTCAAGCACTCGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCTGAGGATAAGACGAAGGTCGAGTTCCCTACCTGACTGAGCTGAGCTGCACTCTATC 60

Qy     61 CCGAACGCGGTGCTCTTGAGTCGAACCTCGGCCTCTCGCTCTACTACGGCCCGGCGGATC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTAAGCTTGCTGTTTGAGTCCACGCTCGGACTCCGGACTCGGACTCTGCCCCGAGCGGATC 120

Qy    121 TTCAACGCGTCGGCGTCGGCCTGCTCGGCGCGTGCTCTCTACGGCGGCCGGTTCATTGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTCAACGCCATCGCCTCGCTCTCGCTCGCTCACGCTGCCCGGATCATCCCCTTCATTGCC 180

Qy    181 GATAACGTTCTGCTCCACGCGCTCGTTTGCGCCACTACGTGCAGGGCGTCATC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATAAGTTCTGTTTGCTTGTTCGTTTGCGGCCACATCTACACATCTACACCAC 240

Qy    241 TTCTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTTCTCGCGCTACCAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTCTGGGGTTTCTTTACCGTCGGCTCACGACTGGTCACGACTGCCGATACCAC 300
```

```
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia declina
US-10-840-325-46

Query Match         81.0%;  Score 872.2;  DB 21;  Length 1077;
Best Local Similarity  88.1%;  Pred. No. 5.1e-237;
Matches  949;  Conservative  0;  Mismatches  128;  Indels  0;  Gaps  0;
```

```
Qy    1  ATGACTGAGGATAAGACAAGGTCGAGTTCCGACGCGTCACGGAGCTCAAGCACTCGATC   60
            |||||||||||||||| |||||||||||||  ||| |||||| |||| ||||||| ||||
Db    1  ATGGCTGAGGATAAGACCAAGGTCGAGTTCCTACCCTGACGTGAGCGAGCACTCTATC   60

Qy   61  CCGAACGCGTGCTTGAGTCGCAACCTCGGCCTCCTACTACACGGCCGCGGCCGGCGATC  120
            || |||||| ||||||||||  ||||| |||  || |||||||||| || ||||| |||
Db   61  CCTAACGCTGCTTGAGTCCAACCTCCGGACTCCTGCTCCGCTCTACTACACTGCCCGAGCGATC  120

Qy  121  TTCAACGGCTCGGCGCGCTGCGTCACGGAGCTGCTTACGGCGCCGTTCATTGCC  180
            |||||||||| |||||||||||||||||| ||||  || |||| ||||||||||||
Db  121  TTCAACGGCATCGCCTGCGTCGTCTGCGTCTCCGATCTCACTCTACTCCCTTCATTGCC  180

Qy  181  GATAACGTTCTGCTCCAGCTACTCCGGCTTTGCGGTCATC  240
            |||||||||||||||||| ||||||||||||||||||||||
Db  181  GATAACGTTCTGCTCCAGCTACTCCGGCTTTGCGGTGTCATC  240

Qy  241  TTCTGGGCCTTCTCACGGTCGGCGCCACGACTGGCGCCCTTCGGCGTTCGGCGGTACCAC  300
            ||||| |||| |||||||||||||||||||| || |||||||||||| |||||  ||||||
Db  241  TTCTGGGGTTTCTTCACGGTCGGTCACTCTGCTCACTCTGCCTTCTCCGTCCCGATACCAC  300

Qy  301  AGGCTCAACTTTATCATCGGCTGCATCATGCGTCGTTGACGCCGTTCGAGAGC  360
            ||||||||||||  ||||||||||||||||||| || |||||||||||||||||
Db  301  TCCGTCAACTTCATCATTGGCTGCATCATGCGTCGTTGACTTCTGACGCCGTTCGAGTCC  360

Qy  361  TGGCGGTGGACGCACCGGTCGGTGGTTGTCAACATTGATAAGGACGAGATC  420
            |||| | || |||||| ||||||||||||||  ||||||| |||| |||||||
Db  361  TGGCGGTGCTCGACCGCGTTCGTGGTTGTCTACCTCGGCAACATTGATAAGGACGAGAGATC  420

Qy  421  TTTTACCCGCACCGGTCGGTCAAGGACTCCAGGAGCCCAATGGGTCTACACGGTC  480
            |||| ||||||||||||| |||||| |||||| || ||||||||||| ||||||||
Db  421  TTCTACCCTCATCGGTTGCCAATCATTCCCATCATTCCCAGGACCTCCAGGGGTCATC  480

Qy  481  GGCGGTGGGACCCGCTCCTCCTTCGCGCGCTCGTACGGCCGCACCCAC  540
            |||||||||| ||||||||||||||||||| ||||||||||||| |||||
Db  481  GGAGGTGCTTGGTTTGTCTACCTGGTACTCCCTGGTACGGCTGACTCGGAGTC  540

Qy  541  GACCCGTGGGACCCGCTCCTTCTTCGCGCCTGGCCTTCACATACTCGGCTTTGCGGTC  600
            |||||||||||||||||||||||| || |||||| |||||| |||| |||||| |||||
Db  541  GACCCCTGGGACCCGCTCCTCTCCGTCCCGTCTCCACATCTCGGCTTTCCGGTC  600

Qy  601  TGGGCCGCCTTCTTCGCGCCGTACGGCGTACCTCACATACTCGGCTTTGCGGTCGTCATG  660
            |||| ||||| |||||||||||||||||||||||| |||| || ||| |||||||||||||
Db  601  TGGGCTGCCTTCTTCCGGTCCTACCGCCTACCTCACATACTCGGCTTTGCGGTGTCATG  660

Qy  661  GGCCTCTACTACTATGCGCCGTCTTTGCTTCGTTCCTCGTCATTACGACCTTC  720
            |||| ||||||||||||| ||||||| |||| |||||||||| |||| ||||| |
Db  661  GGCTCTACTACTATGCTCCTCTTCGTTCCTCGTCATTACTACCTTC  720

Qy  721  TTGCACCACAACGACGAAGCGACGCCGTGGTACGGCGACTGAGTGACGTACGTCAAG  780
            |||| | || ||| |||| || ||||| ||||| |||||||| |||||||||||||||
Db  721  TTGCATCACAACGACGAAGCTGACGCCTCATCAACTTCCGTCGGTTACCTCGGGTACGTCAAG  780

Qy  781  GGCCAACCTCTCGAGCCGTCGACCGCCGTTCGTGGTGGACAACCTGAGCGCCAC  840
            |||||||| ||||||||||||||||| || |||||||| |||| ||||||||||||
Db  781  GGCCAACCTCGAGCTGCTTGGTCGTGCCGATCGTGCTGCTGAGAGCTTCGGCTTCACCAC  840

Qy  841  ATTGGCACGACGCCAGGTCGGCGCCACTGTTCCCGATCATTCCCACTACGAA  900
            |||||||||||| |||||| ||| | |||||||  || |||| |||| |||||
Db  841  ATTGGCACCCACCAGGTCCATCACTTGTTCCCTATCATTCCCACTACAAGCTCAACGAA  900

Qy  901  GCCACCAAGCACTTTGCGCCGGTACCCGCACCTCGTGCGCAGGAACGACGAGCCCATC  960
            |||||||||||||||||||| | | ||||||| ||||||||||||||||||||||||||
Db  901  GCCACCAAGCACTTTGCTGCCGGTTACCCTTACCCTCGGCGCAGGACAGTGTAACGAGCCCATC  960
```

```
Qy  301  AGGCTCAACTTTATCATCGGCTGCATCATGCGTCGTTGACGCCGTTCGAGAGC  360
            |||||||||||| ||||||||||||||||||| || ||||||||||||||||
Db  301  TCCGTCAACTTCATCATTGGCTGCATCATGCGTCGTTGACTTCTGACGCCGTTCGAGTCC  360

Qy  361  TGGCGGTGGACGCACCGGTCGGTGGTTGTCAACATTGATAAGGACGAGATC  420
            |||| | || |||||| ||||||||||||||  ||||||| |||| ||||||
Db  361  TGGCGGTGCTCGACCGCGTTCGTGGTTGTCTACCTCGGCAACATTGATAAGGACGAGAGATC  420

Qy  481  GGCGGTGGGACCCGCTCCTCCTTCGCGCGCTCGTACGGCCGCACCCACTT  540
            |||||||||| ||||||||||||||||||| ||||||||||||| |||||
Db  481  GGAGGTGCTTGGTTTGTCTACCTGGTACTCCCTGGTACGGCTGACTCGGAGTC  540

Qy  541  GACCCGTGGGACCCGCTCCTTCTTCGCGCCTGGCCTTCACATACTCGTGCTCGGCGGTC  600
            |||||||||||||||||||||||| || |||| |||||| |||| |||||| ||||||
Db  541  GACCCCTGGGACCCGCTCCTCTCCGTCCCGTCTCCACATCTCGTGCTCGGCGAGTC  600

Qy  601  TGGGCCGCCTTCTTCGCGCGTACGCGGTACCTCACATACTCGGCTTTGCGGTCGTCATG  660
            |||| ||||| |||||||||||||||||||| |||| ||| ||| ||||||||||||||
Db  601  TGGGCTGCCTTCTTCGCGCTACACTACGGCTTTTGCGGTGTCGTCATG  660

Qy  661  GGCCTCTACTACTATGCGCCGTCTTTGCTTCGTTCCTCGTCATTACGACCTTC  720
            |||| ||||||||||||| |||||| |||| ||||||||||| |||| ||||| 
Db  661  GGCTCTACTACTATGCTCCTCTTCGTTCCTCGTCATTACTACCTTC  720

Qy  721  TTGCACCACAACGACGAAGCGACGCCGTGGTACGGCGACTGAGTGACGTACGTCAAG  780
            |||| | || ||| |||| || ||||| ||||| |||||||| |||||||||||||||
Db  721  TTGCATCACAACGACGAAGCTGACGCCTCATCAACTTCCGTCGGTTACCTCGGGTACGTCAAG  780

Qy  781  GGCCAACCTCTCGAGCCGTCGACCGCCGTTCGTGGTGGACAACCTGAGCGCCAC  840
            |||||||| ||||||||||||||||| || |||||||| |||| ||||||||||||
Db  781  GGCCAACCTCGAGCTGCTTGGTCGTGCCGATCGTGCTGCTGAGAGCTTCGGCTTCACCAC  840

Qy  841  ATTGGCACGACGCCAGGTCGGCGCCACTGTTCCCGATCATTCCCACTACGAA  900
            |||||||||||| |||||| ||| | |||||||  || |||| |||| |||||
Db  841  ATTGGCACCCACCAGGTCCATCACTTGTTCCCTATCATTCCCACTACAAGCTCAACGAA  900

Qy  901  GCCACCAAGCACTTTGCGCCGGTACCCGCACCTCGTGCGCAGGAACGACGAGCCCATC  960
            |||||||||||||||||||| | | ||||||| ||||||||||||||||||||||||||
Db  901  GCCACCAAGCACTTTGCTGCCGGTTACCCTTACCCTCGGCGCAGGACAGTGTAACGAGCCCATC  960

Qy  961  ATCACGGCCTTCTTCAAGAGACCGGCCAACTACACGGGCGTGTGCCCGAGACG 1020
            ||| |||||||| ||||| |||||||||||||| |||||||| |||||||||
Db  961  ATTACTGCCTTCTTCAAGATCCGCTACCGCTACACGGAGCGTGTGCCGACT 1020

Qy 1021  GGCCAGATCTTCACGCTCAAAGAGTCGGCGCCCAAGGCCCAAGAGCCAGTCGGACTAA 1077
            ||||| || |||||| || |||  |||||||||||| ||||||||||||||||||||||
Db 1021  GCTCAGATTTTCACCCTCCCAAAGAGTCTGCGCCGCTTACCCTCCCACCTGCGCAGAGCGACTAA 1077
```

RESULT 9

```
US-10-840-325-46
; Sequence 46, Application US/10840325
; Publication No. US20050043527A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; TITLE OF INVENTION: A DELTA-12 DESATURASE GENE SUITABLE FOR ALTERING LEVELS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN OLEAGINOUS YEASTS
; FILE REFERENCE: CL2301
; CURRENT APPLICATION NUMBER: US/10/840,325
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US 60/484209
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US 60/468677
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
```

Qy 601 TGGGCCGGCCTTCTTCGCGCTGTACGGCTACCTCACATACTCGCTTCGGCTTTGCGTCATG 660
        ||||| |||||||||||||||| | ||||||||||||| ||||||||||||||||||||||
Db 601 TGGGCTGGCCTTCTTCGCGCTGCTCCTACGGCTACCTCACTACTCGCTTCGGCTTTGCGTCATG 660

Qy 661 GGCCTTACTACTATCGCCGTTCTTGTTCTTGTTGTCGTTCCTGTTCGTCGTTCATTACGACCTTC 720
        ||||||||||||||||||||| ||||| ||||||||| ||||| ||||| ||||||||| |||||
Db 661 GGCCTCTACTACTATCGCCGTTCTCCTTGTTCTTGTTGTCGTTCCTGTTCGTCGTTCATTACTACCTTC 720

Qy 721 TTGCACCACACGACGAAGGACGACGAAGCTACTCCCGTACGGACGACTCGGAGTGGACGACTACGTCAAG 780
        ||| || || || |||||| ||||||| |||||||||| ||||||||||||||||||||| |||||
Db 721 TTGCATCACACAGACGAAGCTACTCCCGTACGGACGACTCGGAGTGGACCTACGTCAAG 780

Qy 781 GGCAACCTCGAGCGTCGACCGATGTCGTCGACGAGCTTTCGTCGTCTCTCCACCAC 840
        |||||||||| |||||| |||||||||||||||| ||||||||||||||||||||||
Db 781 GGCAACCTGAGCTCCGTCGACCGATGTCGTCGACGAGCTTTCGTCGTCTCTCCACCAC 840

Qy 841 ATTGGACGCACCAGGTCCACCACTTGTTCCGATCATTCCGCACTACAAGTCAACGAA 900
        |||||||||||| ||||| |||||||||| ||||||||| ||||| ||||||||||||
Db 841 ATTGGCACCACCAGGTCCATCACTTGTTCCTATCATTCCCTACTACAAGTCAACGAA 900

Qy 901 GCCACCAAGCACTTTGGGCGCCGTACCGTACCCGCACCTCGTGCGCCAGGAGAACGACGAGCGCCATC 960
        ||||||||||||| |||||||| ||||| ||||| |||||||||| ||| ||| ||||||||||||
Db 901 GCCACCAAGCACTTTCTGCGCCTTACCCTCACCTCGTGCTGACGTACGACGAGCCCATC 960

Qy 961 ATCACGGCCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGGCGTGTCCCGAGACG 1020
        || | |||| |||||||| ||||||| |||||||||||||||| |||||||||||
Db 961 ATTACTGCCTGTTCTTCAAGAGCGCGCTGCTCCTCTTTGTCAACTACGGAGAGCGTGCCCGAGACT 1020

Qy 1021 GCGCAGATCTTCACGCTTCAAAGAGTCGGCCCGGCCGCCAAGTCGGACTAA 1077
         |||||||||||||| ||| ||||||||| |||||||||||||||||||
Db 1021 GCTCAGATTTTCACCCTTCAAAGAGTCTGCAGCCGACGGCCAAGAGCGACTAA 1077

RESULT 10
US-10-840-579-9
; Sequence 9, Application US/10840579
; Publication No. US2005013651 9A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.
; TITLE OF INVENTION: PRODUCTION OF OMEGA FATTY ACIDS IN OLEAGINOUS YEASTS
; FILE REFERENCE: CL2233 PCT
; CURRENT APPLICATION NUMBER: US/10/840,579
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US 60/468677
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia declina
US-10-840-579-9

Query Match   81.0%;   Score 872.2;   DB 22;   Length 1077;
Best Local Similarity 88.1%;   Pred. No. 5.1e-237;
Matches 949;   Conservative   0;   Mismatches 128;   Indels   0;   Gaps   0;

Qy   1 ATGACTGAGGATAAGACGAAGCTGAGTTCCGAGCTCAGGGAGCTCAAGCACTCGATC 60
         |||||||||||||||||| |||||||||||||||||||| ||||||||||||||||||
Db   1 ATGGCTGAGGATAAGACCAAGGTCGAGTTCCCTACCTGACTGCCTACCCGAGCACTCTATC 60

Qy   61 CCGAACGGCGTGCTTTGAGTCGAACCTGGCCTTCGGCCTTCCGCTCTCGCTCTACTACACGGCCCGCGCGATC 120
         ||||| |||| ||| ||||| |||||||||||||||| |||| |||| ||||||||||||||| ||||||||
Db   61 CCTAAGCGTTGCTTTGAGTCCAACCTCGCCTTCGGCCTCCCGCTCTCGCTCTACTACTGCCGAGCGATC 120

Qy 121 TTCAACGACGTCGGCCTCCTGCCTCTGCCTCTGACGTGTGCTGTCCCGATCTACTCCCTTCATTGCC 180
         ||||||| |||| ||||||||||| ||||| |||||||||||| ||||| ||||| |||||||||||
Db 121 TTCAACGATGTCGGCCTCCTGCCTCTCGCCTCTGCCTCTGACGTGTGCCTGTCCCGATCTACTCCCTTCATTGCC 180

Qy 181 GATAACGTTCTGCTCCACGCGCTCGTTGGCCACTACATCTACGTGCAGGGGGTCATC 240
         ||||| |||||||||||| |||| ||||||||||| |||||||||||||||||||||
Db 181 GATAACGTTCTTCTTTACGCTCCGGTTGCCCACTACTACGTGCAGGTGGTGTCATC 240

Qy 241 TTCTGGGCCTTCTTCACGGTCGGCCACGACGTGCGGCCTTCTGCGGCTTCTGCGCGTACCAC 300
         ||| |||||||||||| |||| |||||| |||||| ||| || |||||||||||||||||
Db 241 TTCTGGGGTTCTTCTTTACCGTCACGACTCGGTGGTCACTCTGCCTTCTCCCGATACCAC 300

Qy 301 AGGGTCAACTTATCATCGGCTGCATCATGCGCATCGGCGATTTTGACGACCTTCGAGAGC 360
         ||| |||||||| |||| |||||||||||| | |||| ||| ||| |||||||||||||||
Db 301 TCCGTCAACTTCATCATTGGTGCATCATGCTGCCATTCTGCCATTGCTGCGATTTTCTGCCATTCTGCGATTTTCGAGTCC 360

Qy 361 TGGCGCGTGACCGAGTCGTGGCTGCTTGTCTACTGGAGGAGAACACGGCCAACATTGATAAGGACGAGATC 420
         ||||| |||||| | |||||| |||||||||| ||||||||||||||||||| ||||||||||| |||||
Db 361 TGGCGGAGGTGCTTTGGTTTGTCTACTGGAGGTCGGAGTCGGATATGCTCTCGAATGCTCTGAATATGGGCAACATGATCATC 420

Qy 421 TTTTACCCGCACCGGTCGTCGGTCAAGGAACCTCAGGACGTGCGCCAATGGGTCTACACGCTC 480
         |||| |||| || ||||| |||| |||||||| |||||| |||||| || ||||||||||||
Db 421 TTCTACCCGCATCGGTCGTCGGTGAAGGAACCTCAGGACACGGGTCTACACGCTC 480

Qy 481 GGCGGTGCGTCGGTTGTCTACTGGCGGGTCGGGTATGCCGCGCCCGGCCGCGATGAGCGCCACTTT 540
         |||||||| |||| || ||||||| ||||||| |||||| | |||| ||||| ||||||||||||
Db 481 GGAGGTGCTTGGTTGTCTACTGGCGGATATGCTCTCGAATGCTCTGAATATGGGTCACCATTCCCACTTT 540

Qy 541 GACCCGTGGGACCGCACGGTCGCGCTCCTTCCTGCTTCCTCGCGTCCTTCGGCTC 600
         ||| |||||||| ||||||| || |||||| || ||||| ||||| |||||||
Db 541 GACCCCCTGGGGACCGCACCGGTCGCTCCTTCGTCTTTCATGTCATGTCCTGTCCCTCGGAGTC 600

Qy 601 ... (continues)

Query Match   80.7%; Score 869.6; DB 22; Length 10328;
Best Local Similarity   88.0%; Pred. No. 4.3e-236;
Matches 947; Conservative   0; Mismatches 129; Indels   0; Gaps   0;

```
Qy      1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCGAGCGTCACGGAGCTCAAGCACTCGATC 60
          |||||||||||||||||| ||||||||||||||||| |||||| ||||||||||||||||
Db   6476 ATGGCTGAGGATAAGACCAAGGTCGAGTTCCCTGACTCGAGCGAGCACTCTATC 6535

Qy     61 CCGAACGGTCGCTTGAGTGCGAACCTCGGCCTTCGCCTCACTACACGCCCCGCGGATC 120
          |||||||| | ||||||||||||||||||||||||||||||||||| |||||| |||||
Db   6536 CCTAACGCTTGTTTGAGTGCGAACCTCGGCCTTCGCCTCACTACACTGCCCCAGCGGATC 6595

Qy    121 TTCAACGGGTCGGCCTCGGCGGCGTCGTCTACGGCGGCGTCGCCGTTCATTGCC 180
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   6596 TTCAACGGCATCTGCCTCGTCGCTCTGCTCTACGGCGTCCCCTTCATTGCC 6655

Qy    181 GATAACGTTCTGCTCCACGCGGTCGTTGCGGCCACCTACGTGCAGGCGGTCATC 240
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   6656 GATAACGTTCTGCTCCACGCTCTGGTTGCGGCCACCTACGTGCAGGCGGTCATC 6715

Qy    241 TTCTGGGGCTCTTCACGGTCGGCGGTGGCCAGGACTGGGGCCACTGGGCCTACCAC 300
          |||||||||||||| |||||||||||||||||||||||||||||| ||||||||||
Db   6716 TTCTGGGGGTTCTTTACCGTCGCTCACGTGGTCACTCGGCGATTTGACGCGGTCGAGAGC 6775

Qy    301 AGGGTCAACTTTATCATCGGCGTCGTGCATCGGCGATTTTGACGCGGTTCGAGAGC 360
          ||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Db   6776 TCCGTCAACTTCAATCATTGGCGTCATCATCACTCTGCACTCTGCCATTCTGAGTCC 6835

Qy    361 TGGCGGCTGACCGACCCACCGGCAACATTGATAAGGACGAGATC 420
          |||||||||| |||||||||||||||| |||||||||||||||
Db   6836 TGGCGAGTGACCCCGGCAACATTGATAAGGACGAGAGATC 6895

Qy    421 TTTTACCCGCACCGGTCGGTTGTCACTTGAAGTCGGGTATGCCCCGCACGATGAGCCACTTT 480
          |||||||| |||||||| |||||||||| | |||||||||||||||||||||||||||
Db   6896 TTCTACCCTCATCGGTCCGTCAAGGACCTCGGCGACGTGCGCAATGGGTCTACACGCTC 6955

Qy    481 GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGATATGCTCGGCTCATCGTGTCTCGGCGTC 540
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   6956 GGCGGGTCGTGGTTTGTCTACTTGAAGGTCGGATATGCTGTACGCTGTACACCCTC 7015

Qy    541 GACCCGTGGGACCCGTCATCGTGGTTTGGCTTTGCGTCCCTCGGAGTC 600
          ||||||||||| |||||||||||||||||||||||||||||||||||
Db   7016 GACCCCTGGGACCTCTCGCTTCGACGAGTCGGATATGCTTCCTGACGCCCATC 7075

Qy    601 TGGGCCGGCCGCTCTTCGCCGCCGCTCTTGCGTCCCTCGGCTTTGCGTCATG 660
          |||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   7076 TGGGCTGCCTTCGCCGCCGCTCTTCGCGGCCTCGGCTTTGCGTCATG 7135

Qy    661 GGCCTCTACTACTACTATGCGGCGCCGCTCTTTGTCTTCGTTCGTCATTACTACCTTC 720
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   7136 GGCCTCTACTACTACTATGCTCGGCCGCTCTTTGTCTTCGTTCGTCATTACTACCTTC 7195

Qy    721 TTGCACCACAACGACGAAGCGACGCCGTGGAGTGGACGTACGTCAAG 780
          |||||||| ||||||||| ||| |||||||||||||||||||||||
Db   7196 TTGCATCACAACGACGAAGAGCGCTGGGTTGTTCACTGACGTGACTCAAG 7255

Qy    781 GGCGGAACCTCTGCACGCGGTCGTGACCGGCCGTTCTGGTGTACGGCGTCGACCACTT 840
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7256 GGCAACCTGAGCTCCGTCGACATCGTACGCGAAGCTTTCGTGACAACCTGTCTCACCAC 7315

Qy    841 ATTGGCACCCACCAGGTCATTCCCGATCATTCCCACTACACAAGCTCAACGAA 900
          |||||||||| |||||||||||||||||||||||| |||||| ||||||||||
Db   7316 ATTGGCACCCACCAGGTCATTCCCATCATTGTTCCCACTACACAAGCTCAACGAA 7375

Qy    901 GCCACCAAGACACTTTGCGGCGCTACCCGCACCTCGTGCCCAGGAACGAGAGCCATC 960
          ||||||||||||||||||||||| |||||||||| ||||||||||||||||||||
Db   7376 GCCACCAAGCACACTTGCTGCCGCTTACCTCGAGACGCCTAACGACGAGCCCATC 7435

Qy    961 ATCACACGGCCTTCTTCAAGAGACCGGCCGTGTGCCGGACACG 1020
          ||||||||| ||||| ||| |||||||||||||||||||||
Db   7436 ATTACTGCCTTCTTCAAGAGACCGCTCAACCTACCGAGCTGTGCCCCGGAGACT 7495

Qy   1021 GCGCGAGATCTTCACGCTCAAAGAGTCGGCCGCCAGGCCAAGTCGACTA 1076
          || |||||||||| || ||||| ||| | |||| |||||
Db   7496 GCTCAGATTTTCACCCTCAAAGAGTCGCCGCTGCAGCCAAGGCCCAAGAGAGCGACCA 7551
```

RESULT 12
US-10-840-579-101
; Sequence 101, Application US/10840579
; Publication No. US2005013651 9A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.
; TITLE OF INVENTION: PRODUCTION OF OMEGA FATTY ACIDS IN OLEAGINOUS YEASTS
; FILE REFERENCE: CL2233 PCT
; CURRENT APPLICATION NUMBER: US/10/840,579

```
Qy   841 ATTGGGACGCACCAGTCCACCACTTGTTCCCGATCAATTCCGCACTACAGCTCAACGAA 900
         ||||||| |||||||||||| ||||||||||| |||||| |||||||||| ||||||||
Db  7316 ATTGGGCACCCACCAGTCCATCACTTGTTCCCTATCATTCCCCACTACAAGCTCAACGAA 7375

Qy   901 GCCACCAAGCACTTTGCGGCCGTACCCGGCGCGTCGCTGCCGCACCTCGCCGCTACCCTC 960
         |||||| ||||||||||||| ||||| ||||||||||| ||||| ||||| ||||  |||
Db  7376 GCCACCAAGCACTTTGCTGCCCTTCACCCTCGTGCGACTCGCTCTTTGTCAACTCAGCCATC 7435

Qy   961 ATCACGGCCTTCTTCAAGACCGCGACTCTTTGTCAACTACGGCGCTGTGCCCGAGACG 1020
         ||||| ||||||||||||||    ||||||| |||||| |||||||| |||||||||
Db  7436 ATTACTGCCTTCTTCAAGACCTCACTCCTCTTTGTCAACTACGGCGCTGTGCCCGAGACT 7495

Qy  1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCGCCGGCGCCCAAGGCCAAGTCGGACTA 1076
         |||||||||||||| ||| ||||| |||| ||||| ||||||||||||| |||
Db  7496 GCTCAGATTTTCACCCTCAAAGAGTCTGCCCGCAGCCAAGGCCAAGAGCGACCA 7551
```

RESULT 13
US-11-021-712-29
; Sequence 29, Application US/11021712
; Publication No. US20050112719A1
; GENERAL INFORMATION:
; APPLICANT: Roessler, Paul
; APPLICANT: Matthews, T. Dave
; APPLICANT: Ramseier, Tom
; APPLICANT: Metz, James
; TITLE OF INVENTION: Product and Process for Transformation of Thraustochytriales
; TITLE OF INVENTION: Microorganisms
; FILE REFERENCE: 2997-23
; CURRENT APPLICATION NUMBER: US/11/021,712
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US/10/124,807
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,116
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 29
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)..(1228)
; OTHER INFORMATION:
US-11-021-712-29

Query Match   14.7%; Score 158.6; DB 23; Length 1263;
Best Local Similarity   52.2%; Pred. No. 1.2e-34;
Matches   434; Conservative   0; Mismatches 380; Indels   18; Gaps   3;

```
Qy   203 TCGTTTGCGCCACCTACATCTACGTGCGAGGGCGTCATCTTCTGGGGCTTCTTCACGGTCG 262
         ||||| |||| |||||| ||| |||| ||||| ||||| |||||||||||||||||||
Db   327 TCGGCTACCTCGTCTGCGAACATCTTCATGGGCGTCTTCGGCGTTCGCCCTCTTCGTCGTCG 386

Qy   263 GCCACCAGCTCGGGGCCACTCGGCCTTCGCCTTCGGCCTACCACAGCAGGTTCAACTTTA 322
         |||||| || ||||| |||| || ||  |||||||||||  ||||||||  ||| |||
Db   387 GCCACGACTGCCTCACGCGGAGAGCTTCTCGAACAACCAGAACCTCAACGACTTCAACGGCC 446

Qy   323 GCATCATGCACTCTGCGATTTTGACGCCGTTCGAGACGCTTCGAGAGCTGCCGCCACC 382
         |||| ||| ||| ||| |||||| || ||||| || || |||||||||||
Db   447 ACATCGCCTTCGACGCTCTTCTTCGCCCTCACTTCCCCTGCAGAGAAGTCGCACAAGCTCC 506

Qy   383 ACCAAGAGACACGGGCAACATTGATAAGGA-------CGAGATCTTTTACCCGCACCGGT 436
         |||||||||| |||||||| ||||||| |       |||| ||| ||| ||||||||
Db   507 ACCACCGCCTTCACCAACCACATCGACAAGGACCACCGGCCACACGCTCGCCTCATCAGG 566

Qy   437 CGGTCAAGGACTTCAGGACGGCTGCGCGCAATGGCGTGCACGGGTCTACAACGGCTTA 496
         |||||| ||||||  ||| || ||  ||||| |||| |||||| ||||||||||||||
Db   567 ACTGGGAGGCCATGCCCTCGTGGAAGCGCGTGGTCGTTCAACCCCATCCCTTCTCGGGCTGGC 626

Qy   497 TCTACTTGAAGTGCGGGTATGCCCCGCGCACGATGAGC------CACTTTGACCCGT 547
         |||| || ||||||| |||| || |||||||||||| |      |||||| |||||
Db   497 TCTGCTTCTACCTCGCCGACCACCTCGCCGCATCG------CGCCGGGGGCTCGTTTGCGCC 213
```

RESULT 14
US-10-604-708-10
; Sequence 10, Application US/10604708
; Publication No. US2004022135A1
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, Christine K
; APPLICANT: Van Eenennaam, Alison
; APPLICANT: Hawkins, Debra T
; APPLICANT: Sanders, Rick
; TITLE OF INVENTION: Methods for Increasing Total Oil Levels in Plants
; FILE REFERENCE: 38-77(52794)
; CURRENT APPLICATION NUMBER: US/10/604,708
; CURRENT FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: US 60/402,527
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Zea mays
US-10-604-708-10

Query Match   10.5%; Score 113.2; DB 20; Length 1543;
Best Local Similarity   48.1%; Pred. No. 9.3e-22;
Matches   478; Conservative   0; Mismatches 453; Indels   63; Gaps   3;

```
Qy   627 TCAAGTGGTTCCCGTCTACACCCTCTTCGGGCTTCTGCGACGGCTCGGCACTTCTGGCCCT 686
         ||||||| |||| | |||| ||| |||||| ||| || ||||| || || |||||||||
Db   548 GGGACCCGCTCCTCCTTCGTCCGCGTCGGCGTCATCGTGTCGCTGCTCGGCGTCTGGGGCCG 607

Qy   687 ACTCGTCGTCGTCTTCGTCCGCCAACTCGGAGACGCGGTCGATCTGCTC 746
         |||||| |||  ||| ||| | |||||||| || || |||| |||| |||
Db   608 CCTTCTTCGCCGTACGGCGTACCTCACATATCGGCTCTCGGCTTGCGTCATGGGCCTCT 667

Qy   747 GCTGCGGTCTGCGGCTACGGCTACATCGGCCTCGTCGTTCCTCGTCGTCGTTTCTGCAC 806
         |||||| |||||| |||||||| |||||| |||||||||| ||| |||||||||||||
Db   668 ACTACTATGCGGCCGCGGCTCTTGTCTTGTTCGGCCCTCGTCTTCGTCGTCGTTCTGCAGC 727

Qy   807 ACTACTGGGTCCCGCTCTCGTTCTTGTCGTTCTTCGTGTAGCGCGACTCGGACGTACGGC 866
         || |||||| |||| ||||||| || || |||| ||||| ||||||| |||||||||||
Db   728 ACAACGACGAAGGACGCCGTGTGACGGCCGAGGCGACGACGGTGGTCGTCGTTGTCCGGCCACC 787

Qy   867 AGTCGACGACGTCGCCGAGTCGTACGAGGCGGTCTACGAGGGCGGTCGTTGTGTCCGGGCCAGA 926
         ||||||||||| ||| || ||||||| || |||| ||| ||||||||||||||||
Db   788 TCTCGAGGCGTCGACCGCTCGTACGGGGCGGTTCGTGGACAACCTGAGCCACCACAT---TG 844

Qy   927 CCCAGACCATCGACCGGCTACTACGGCCTCCGGCCTCGGCCTCGACGCTCGACCACCATCACCG 986
         |||||||||| |||| |||||||| ||| ||||||||||||||| |||||||||||| |||
Db   845 GCACGGCACCAGGTCCACCACTGTTCCCGATCATTCCGCACTACAAGCTCAACGAAGCCA 904

Qy   987 ACGGGCCACCAGTCGCCACCACCTTCTTCAACAAGATCCCGCACTACCACCTCATCGAGGGCCA 1046
Db   905 CCAAGCACTTTGCGGCCGCTCGTACCCCGGTACCGCACCTCGTGCGGCAGCGAGCGAGCCCATCATCA 964

Qy  1047 CCGAGGGGCGTCAAGAAGGTCCTCGAGCCCCTTCGAGCACCCCAGTACGGCTACAAGTCGC 1106
Db   965 CGGGCCTTCTTCAAGACACTTCTTGCGCCGCTTCCTCTGGTTCAACTACAAGCTCGA 1016

Qy  1107 AGTCAACTACGACTTCTTCGCCGCTTCCTCTGGTTCAACTACAAGCTCGA 1158
```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 68012
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68816C.1
US-10-437-963-68012

Query Match   10.5%;   Score 113;   DB 19;   Length 1317;
Best Local Similarity 49.8%;   Pred. No. 1e-21;
Matches   413;   Conservative   0;   Mismatches 365;   Indels 51;   Gaps   3;

Qy   191 TGCTCCACGCGCTCGTTTGCGCCACCTACATCTACGTGCAGGGCGTCATCTTCTGGGGCT 250
          ||||||||||||||||||||||||||||||||| |||| ||||||||| || |||||||
Db   407 TCCTCCGCGTCGTCGCCTGGCCGCCTCTACTGGCGCCGCCCAGGCGAGTGTACTACCGGCG 466

Qy   251 TCTTCACGGTCGCGCCACGACTGCGCGCCACTCGGCCTTCTCGCCGTCGACCAGCGTCAACT 310
          ||||||||||||| |||||||| ||||||||||||| |||||||||||||||||||||||
Db   467 TGTGGGTCATCGGCACGAGTGTGCCACCACCTGCGCCTTCTCGGACTACTTGCTCCTCGACA 526

Qy   311 TTATCATCGGCTCGTCATCATGCGACCTCTGCGATTTGACCGCCGGTTCGGAGAGCTGCGCGTGA 370
          ||| |||||||| |||||||| |||| ||| ||||||||||||||
Db   527 ACCTCGTGGCCTAGTGCTCCACTCCCGGCGCTTCTCACGGCCCTTCTTCTCGTGGAAGTACA 586

Qy   371 CGACCGGCCACCACCAGAACACGGGCAACATTGATAAGGACGAGATCTTTTA----- 425
          |||||||||||||||||||||||||||||||
Db   587 GCCACCGGCGGCGACCACCGCCAACACCGGCTCATGGACGAAAGACGAGGTGTACGTCGGCGA 646

Qy   426 ---------------------------------CCCGGCACCGGTCGGTCAAGGACCTCCAGGACG 457
Db   647 AGAGAAGTCCGGCGCCTGGTGTACACGCGTCGCGTGGTTGTTCTCACTTGAAGGTCGG----- 706

Qy   458 TGGCGCCAATGGGTCTACAGCGTGCGCGCCGGTGGCGTGGTACGGGAC 512
          || |||||||||||||| |||||||||||||||||||||||
Db   707 TGGTGTACATGCCCCTGCCAGCTCACCTCGGCGTGGCCACTCTACCTCGCGTTCAACCTGT 766

Qy   513 --------GTATGCCCCGCGACGATGAGCCACTTTGACCCGCTGGGACCGCTCCTCC 562
Db   767 CCGGGCAGCCGTACCCACGCGCCTCGAGCGTGCCACACCCCCTACAGCCCGCTGTTCA 826

Qy   563 TTCGCCCGCCGTCGGCC---GTCATCGTGTCGTCGGCGTCGGCGCTCCGCCCTTCTTCGCCG 619
          || |||||||| |||
Db   827 GCGACCAGGAGCGCGTCCAAGTCCTCGTCTCCGACGCGCCCATCCTGGCCGTGCTCG 886

Qy   620 CGTACGCGTACCTCCACATACTCGCTCGGCCTTTGCCGCTGGTGGTGGCCTTCTACTATGCGC 679
          || |||||||||||||||| |||||
Db   887 CCGTGACAGGTGACGGCGGCTACGGCGTCTTGTCGGCGTGTACGGCGTGC 946

Qy   680 CGGTCTTTTGTCTTTGCTTCGTCCGTCATTACGACCTTCTATTACGACCTTCTCATTACGACGAAG 739
          || ||||||||||||
Db   947 CGGTGATGATGATCGTGGTGGGGCCGTGTTCGTGCTCATCACGTACCTACCTCACCACCGGG 1006

Qy   740 CGACGCGTGGTACGGGACTCGGAGTGGACGTGGACGTGGCGTCGCGCTCCGAGCGTCG 799
          || |||||||||||||||||||||||||||||||
Db   1007 CGCTCCCGCCACTACGACTCCAGCGAGTGGATGGCTCGCTCGGCGTGG 1066

Qy   800 ACCGGCGTCGTACGGCCGCGTCCTCCAACCGCCGTGCTCGACAACCGCGTTGCGG 859
          |||||| |||||||||
Db   1067 ACCGGGACTACGGCGTCTCCAACCCGCCGTGCTGCAACGCACGCAGCTCCTCC 1126

Qy   860 ACCACTTGTTCCCGATCATTCCGACTACAAGCTCAACGAAGCCACCAGCACACTTTGCGG 919
          |||||| |||||
Db   1127 ACCACCTCTTCCCCAGCATGCCACACTACCACCGCCATCATGCCCATCATCACGGC 1186

Qy   920 CCGCGTACCCGCACCTCGTGCCGCAGGAACGACGAGCCCATCATCACGGC 968
          ||||||||||||||
Db   1187 CCGTCCTCGTGAGTACTACAAGTTGACCGCGCCCATCATCGAGGC 1235

RESULT 15
US-10-437-963-68012
; Sequence 68012, Application US/10437963
; Publication No. US2004012334341
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

Tue Oct 11 13:05:42 2005

us-10-060-793a-25.rnpb

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005   Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:    October 11, 2005, 07:57:32 ; Search time 4887 Seconds
                                         (without alignments)
                                       10678.590 Million cell updates/sec

Title:          US-10-060-793A-25
Perfect score:  1077
Sequence:       1 atgactggataagacgaa.........ccaaggccaagtcggactaa 1077

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       4708233 seqs, 2422607955 residues
Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
```

Database :   GenEmbl:*
```
1:  gb_ba:*
2:  gb_htg:*
3:  gb_in:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Score	Length	DB	ID	Description				
1	1077	100.0	1077	8	AY373823	AY373823 Saprolegn		100	9.3	1733 6	BD234746 Desaturas
2	157	14.6	2090	6	E49240	E49240 Omega 3 fat		99.6	9.2	1856 6	AK065239 Oryza sat
3	133	12.3	2485	1	SPU36389	U36389 Synechococc		98.6	9.2	1203 8	AF417244 Mortierel
4	131.2	12.2	1988	8	AB075527	AB075527 Chlorella		98.6	9.1	1203 8	AF417245 Mortierel
5	113	10.5	1089	6	AX653555	AX653555 Sequence		97.6	9.1	1725 1	SYCDESB D13780 Synechocyst
6	113	10.5	1267	8	AK105371	AK105371 Oryza sat		97.6	9.1	143308 1	D90913 Synechocyst
7	113	10.5	154025	8	AP005168	AP005168 Oryza sat		96	8.9	2247 8	AB007640 Chlamydom
8	109.6	10.2	1518	8	D43688	D43688 Triticum ae		94.4	8.8	1590 8	D84678 Triticum ae
9	107.2	10.0	1549	6	E38843	E38843 Microsome 1		93.8	8.7	1427 8	AB075526 Chlorella
10	107.2	10.0	1595	6	E11610	E11610 cDNA encodi		93.6	8.7	302550 1	AP006581 Gloeobact
11	107	9.9	1182	8	AY373822	AY373822 Saprolegn		93.4	8.7	1302 1	AF134896 Gloeobact
12	107	9.9	1811	8	AK071185	AK071185 Oryza sat		93.4	8.7	297850 1	AP006577 Gloeobact
13	105.8	9.8	662	6	E49247	E49247 Omega 3 fat		92.8	8.6	1177 8	AK061506 Oryza sat
14	102.6	9.5	1494	8	D63953	D63953 Zea mays FA		91.6	8.5	1146 6	BD235521 Desaturas
15	102.2	9.5	1612	8	AK098930	AK098930 Oryza sat		91.6	8.5	1790 6	BD234745 Desaturas
16	102.2	9.5	1617	8	AK061531	AK061531 Oryza sat		91.6	8.5	1790 6	AR207489 Sequence
17	101.2	9.4	1700	8	AK072282	AK072282 Oryza sat		91.6	8.5	6337 6	BD235520 Desaturas
c 18	101.2	9.4	123428	8	AP004098	AP004098 Oryza sat		91.6	8.4	1245 6	AX654569 Sequence
c 19	101.2	9.4	172832	8	AP004047	AP004047 Oryza sat		90.8	8.4	1297 6	AF182521 Momordica
20								100	9.3	1733 6	BD234746 Desaturas
21								99.6	9.2	1856 6	AK065239 Oryza sat
22								98.6	9.2	1203 8	AF417244 Mortierel
23								98.6	9.1	1203 8	AF417245 Mortierel
24								97.6	9.1	1725 1	SYCDESB
25 c								97.6	9.1	143308 1	D90913 Synechocyst
26								96	8.9	2247 8	AB007640 Chlamydom
27								94.4	8.8	1590 8	D84678 Triticum ae
28								93.8	8.7	1427 8	AB075526 Chlorella
29 c								93.6	8.7	302550 1	AP006581 Gloeobact
30								93.4	8.7	1302 1	AF134896 Gloeobact
31								93.4	8.7	297850 1	AP006577 Gloeobact
32								92.8	8.6	1177 8	AK061506 Oryza sat
33								91.6	8.5	1146 6	BD235521 Desaturas
34								91.6	8.5	1790 6	BD234745 Desaturas
35								91.6	8.5	1790 6	AR207489 Sequence
36								91.6	8.5	6337 6	BD235520 Desaturas
37								90.8	8.4	1245 6	AX654569 Sequence
38								88.4	8.2	1297 6	AF182521 Momordica
39								88.4	8.2	1308 6	BD224596 Genes for
40								85.8	8.0	1403 8	AB020033 Mortierel
41								82.8	7.7	1037 8	AY581826 Cynodon d
42 c								82.4	7.7	110000 8	AE016819_14 Continuation (15 o
43								82	7.6	1200 6	BD232181 Compositi
44								82	7.6	1488 6	AR080599 Sequence
45								82	7.6	1488 6	AR098440 Sequence
```

ALIGNMENTS

```
RESULT 1
AY373823
LOCUS       AY373823                1077 bp    mRNA    linear   PLN 05-MAY-2004
DEFINITION  Saprolegnia diclina omega-3 fatty acid desaturase (sdd17) mRNA,
            complete cds.
ACCESSION   AY373823
VERSION     AY373823.1  GI:38426732
KEYWORDS    .
SOURCE      Saprolegnia diclina
  ORGANISM  Saprolegnia diclina
            Eukaryota; stramenopiles; Oomycetes; Saprolegniales;
            Saprolegniaceae; Saprolegnia.
REFERENCE   1  (bases 1 to 1077)
  AUTHORS   Pereira,S.L., Huang,Y.S., Bobik,E.G., Kinney,A.J., Stecca,K.L.,
            Packer,J.C. and Mukerji,P.
  TITLE     A novel omega3-fatty acid desaturase involved in the biosynthesis
            of eicosapentaenoic acid
  JOURNAL   Biochem. J. 378 (Pt 2), 665-671 (2004)
  PUBMED    14651475
REFERENCE   2  (bases 1 to 1077)
  AUTHORS   Pereira,S.L., Mukerji,P. and Huang,Y.-S.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-2003) 104060, Abbott Laboratories-Ross Products
            Division, RP4-3, 3300 Stelzer Road, Columbus, OH 43219, USA
FEATURES             Location/Qualifiers
     source          1..1077
                     /organism="Saprolegnia diclina"
                     /mol_type="mRNA"
                     /strain="ATCC 56831"
                     /db_xref="ATCC:56831"
                     /db_xref="taxon:112098"
     gene            1..1077
                     /gene="sdd17"
     CDS             1..1077
                     /gene="sdd17"
                     /note="SDD17; involved in desaturation of n-6 fatty acids"
                     /codon_start=1
                     /product="omega-3 fatty acid desaturase"
                     /protein_id="AAR20444.1"
                     /db_xref="GI:38426733"
                     /translation="MTEDKTKVEFPTLTELKHSIPNACFESNLGLSLYYTARAIFNAS
                     ASAALLYAARSTPFIADNVLLHALVCATYIVQGVIFWGFFTVGHDCGHSAFSRYHSV
```

NFIIGCIMHSAILTPFESWRVTHRHHHKNTGNIDKDEIFYPHRSVKDLQDVRQWVYTL
GGAWFVVLKVGYAPRTMSHFDPWDPLLLRRASAVIVSLGVWAAFFAAYAYLTYSLGPA
VMGLYYYAPLFVFASFLVITTFLHHNDEATPWYGDSEWTYVKGNLSSVDRSYGAFVDN
LSHHIGTHQVHHLFPIIPHYKLNEATKHFAAAYPHLVRRNDEPIITAFFKTAHLFVNY
GAVPETAQIFTLKESAAAAKAKSD"

ORIGIN

Query Match   100.0%;   Score 1077;   DB 8;   Length 1077;
Best Local Similarity   100.0%;   Pred. No. 1.3e-163;
Matches 1077;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy     1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGAGCACTCGATCTCAAGCACTCGATC   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGAGCACTCGATCTCAAGCACTCGATC   60

Qy    61 CCGAACGCGTCGTTTGAGTCGAACCTCGGCCTCTCGCTCTACACACGGCCCGGCGATC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCGAACGCGTCGTTTGAGTCGAACCTCGGCCTCTCGCTCTACACACGGCCCGGCGATC  120

Qy   121 TTCAACGCGTCGGCCTCGGCGCGGCCTCTACGCGGGCGGCGTTGACGCGCCGTTCATTGCC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTCAACGCGTCGGCCTCGGCGCGGCCTCTACGCGGGCGGCGTCGACGCGCCGTTCATTGCC  180

Qy   181 GATAACGTTCTGCTCCACGCGTCGTTGGCCACCTACATCTACGTGCAGGGCGTCATC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATAACGTTCTGCTCCACGCGTCGTTGGCCACCTACATCTACGTGCAGGGCGTCATC  240

Qy   241 TTCTGGGGCTTCTTCACGGTCGGCCACGACTCGGCCACTCGGCCTTCGCGCTACCAC  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTCTGGGGCTTCTTCACGGTCGGCCACGACTCGGCCACTCGGCCTTCGCGCTACCAC  300

Qy   301 AGCGTCAACTTTATCATCGGCTGCATCATGCACTCTGCGATTTTGACGGCCGTTGAGAGC  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGCGTCAACTTTATCATCGGCTGCATCATGCACTCTGCGATTTTGACGGCCGTTGAGAGC  360

Qy   361 TGGGCCGTGACGACGCACCGCCACCACCAAGAACACGGGCAACATTGATAAGGACGAGATC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TGGGCCGTGACGACGCACCGCCACCACCAAGAACACGGGCAACATTGATAAGGACGAGATC  420

Qy   421 TTTTACCCGCCACCGGTCGGTCAAGGACCTTCCAGGACGTGCGCCAATGGGTCTACACGCTC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTTACCCGCCACCGGTCGGTCAAGGACCTTCCAGGACGTGCGCCAATGGGTCTACACGCTC  480

Qy   481 GGCGGTGCCGTGGTTTGTCTACTTGAAGGTCGGGTAAGGTCGGGTATGCCCCGCCACGAGCGCACTTT  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGCGGTGCCGTGGTTTGTCTACTTGAAGGTCGGGTAAGGTCGGGTATGCCCCGCCACGAGCGCACTTT  540

Qy   541 GACCCGTGGACCTGGGCAACCGGACCCGGCCGTCCTTCGCGCCGTCATCGTGTCGCGCTGGCGGTC  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GACCCGTGGACCTGGGCAACCGGACCCGGCCGTCCTTCGCGCCGTCATCGTGTCGCGCTGGCGGTC  600

Qy   601 TGGGCGCCTTCTTCGCGGCGTACACTCGCTCGGCGTTTGCCGTCATG  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGGGCGCCTTCTTCGCGGCGTACACTCGCTCGGCGTTTGCCGTCATG  660

Qy   661 GCTCTACTACTATGCGCCGCTCTTTTGTCTTGCTTCGTTCCTCGTTCATTACGACCTTC  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGATGTGGGCGTTGTGCGGCGGCCATCGCCCTCTACTACGGCCATCGACACCCCCTGGT  720

Qy   721 TTGCACCCAACGACGAAGGACGACCCGGTACGGCCGGACTCGGAGTCGGACGTACGTCAAG  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CTGGCCTCTGTACTCGGTGTTGCCCAGGCACGTGGCACCCATGTTCGGCGTCTCGTTCGGGGGCCA  780

Qy   781 GGCAACCTCGAGCGTCGACCGGTCGACGCGTCGACGCGTCGACGCCGGACAACCTGAGCCACCAC  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CGACTGCGGCCACCAGTCCTTCTCCAACGCACAAGGCCCTGAACGACTTTGTGGGCAACAT  840

Qy   841 ATTGGCACGCACCAGGTCACCACTTGTTCCCGACGTCATCATTCGGCACTACAAGCTCAACGAA  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CGTGCACTCCTCCATCACGTGCCCTATCACGGATGGCGCATCAGCCACCACCACCACCA  900

Qy   901 GCCACCAAGCACTTTGCGGCCCGCCACCTCGTGCGGCGCAGGAACGACGAGCGCCCATC  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db   901 GCCACCAAGCACTTTGCGGCCCGCCACCTCGTGCGGCGCAGGAACGACGAGCGCCCATC 960

Qy   961 ATCACGGCCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGGCGCCGTGCCCGAGACG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATCACGGCCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGGCGCCGTGCCCGAGACG 1020

Qy 1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCGGCCGCCGCCAAGGCCAAGTCGGACTAA 1077
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCGGCCGCCGCCAAGGCCAAGTCGGACTAA 1077

RESULT 2

LOCUS   E49240
E49240   2090 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION   Omega 3 fatty acid unsaturation enzymatic gene and utilization
      thereof.
ACCESSION   E49240
VERSION   E49240.1   GI:22553418
KEYWORDS   JP 2001095588-A/1.
SOURCE   unidentified
  ORGANISM   unidentified
           unclassified.
REFERENCE   1 (bases 1 to 2090)
  AUTHORS   Muranaka,T. and Murakami,T.
  TITLE   Omega 3 fatty acid unsaturation enzymatic gene and utilization
  JOURNAL   Patent: JP 2001095588-A 1 10-APR-2001;
           RES INST OF INNOVATIVE TECHNOL FOR THE EARTH, SUMITOMO CHEM CO LTD
COMMENT   OS   Chlorella sp. MK201
           PN   JP 2001095588-A/1
           PD   10-APR-2001
           PF   03-DEC-1999 JP 1999344447
           PI   TOSHIYA MURANAKA,TADAKAZU MURAKAMI
           PC   C12N15/09,C12N1/21,C12N5/10,C12N9/88,C12Q1/68//(C12N15/09, PC
           C12R1:89),
           PC   (C12N9/88,C12R1:91),(C12N5/10,C12R1:19),C12N15/00,C12N5/00, PC
           (C12N15/00,C12R1:89)
           CC
FEATURES   FH   Key   Location/Qualifiers
           FT   CDS   (3)..(1280).
  source   Location/Qualifiers
           1..2090
           /organism="unidentified"
           /mol_type="genomic DNA"
           /db_xref="taxon:32644"
ORIGIN

Query Match   14.6%;   Score 157;   DB 6;   Length 2090;
Best Local Similarity   53.0%;   Pred. No. 9.9e-16;
Matches 455;   Conservative   0;   Mismatches 365;   Indels   39;   Gaps   4;

```
Qy    87 CGGCCTCTGCTCCTACTACACGGCCCGGCGATCTTCAACGCGTCGGCGCTCGGCGGCGCT  146
         |||||||||||  ||||||||||||  ||||||| ||||||  ||||  |||||||
Db   257 CGCCATCCCCAACGAGTGCTTCGAGAAGGACACCTTCGCGTCCGTGGCCACCTGGCCCCT  316

Qy   147 GCTCTACGCGGCGCCGCTCGACGCCGTTCATTGCCGACGCCTTCATTACGACGACCTTC  206
         ||||||||  ||||||||  |||| |||||  ||||||||||||||||||||||||
Db   317 GGATGTGGGCGTTGTGCGGCGGCCATCGCCCTCTACTACGGCCATCGACACCCCCTGGT  376

Qy   207 TTGCGCCCACTACATCTACGTGCAGGGCGTCATCTTCTGGGGCTTCTTCACGGTCGGCAAG  266
         |||||||||||||||||||||  |||||  |||||||||||||||||||||  ||
Db   377 CTGGCCTCTGTACTCGGTGTTGCCCAGGCACGTGGCACCCATGTTCGGCGTCTCGTTCGGGGGCCA  436

Qy   267 CGACTGCGGCCACTCGGCCTTCGGTGGACGGCGGTTCGTGGACAACCTGAGCCACCAC  326
         ||| |||||||||||  |||||||  ||||||||||||||  |||||||||||
Db   437 CGACTGCGGCCACCAGTCCTTCTCCAACGCACAAGGCCCTGAACGACTTTGTGGGCAACAT  496

Qy   327 CATGCACTCTGCGATTTTGACGGCCGTTGACGCGTCGCTATCACGGATGGCGCATCAACGAA  386
         ||||||||||  |||| ||||  |||||||||| |||||||  ||||||||
Db   497 CGTGCACTCCTCCATCACGTGCCCTATCACGGATGGCGCATCAGCCACCACCACCACCA  556

Qy   387 CAAGAACACGGGCAACATTGATAAGGACGAGATCTTTTACCC---------------  428
         ||||||| ||||||||||  |||||||||||||
Db   557 CGCCAACACGGCCAACGGTGGAGACCGACGAGCTGCTGCTGCTACCCCCACCACCAAGTCCAACTA  616
```

OM nucleic - nucleic search, using sw model

```
            GenCore version 5.1.6
     Copyright (c) 1993 - 2005  Compugen Ltd.
```

Run on: October 11, 2005, 07:58:42 ; Search time 4079 Seconds
               (without alignments)
               10050.311 Million cell updates/sec

Title: US-10-060-793A-25
Perfect score: 1077
Sequence: 1 atgacgaggataaagacgaa..........ccaaggccaagtcggactaa 1077

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 3239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
               1: gb_est1:*
               2: gb_est2:*
               3: gb_htc:*
               4: gb_est3:*
               5: gb_est4:*
               6: gb_est5:*
               7: gb_est6:*
               8: gb_gss1:*
               9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Match Length	DB	ID	Description
	1	357.4	33.2	664	7	CF840561	CF840561 psHB009xD
c	2	273	25.3	597	7	CF850773	CF850773 psMA015xP
	3	240.2	22.3	643	2	BE777235	BE777235 MY-26-A-1
	4	222.8	20.7	683	2	BE776116	BE776116 MY-11-B-0
	5	111.2	10.3	1520	3	AY107103	AY107103 Zea mays
	6	102.8	9.5	714	7	CF866439	CF866439 tric006xi
	7	102.8	9.5	770	6	CB896410	CB896410 tric006xi
	8	101.6	9.4	1636	3	AY111307	AY111307 Zea mays
	9	101.4	9.4	700	7	CF877405	CF877405 tric075xp
c	10	101.4	9.4	744	7	CF866831	CF866831 tric008xf
	11	101.4	9.4	754	6	CB905755	CB905755 tric075xp
c	12	101.4	9.4	799	6	CB896826	CB896826 tric008xf
	13	101.2	9.4	749	9	BM076378	BM076378 TrEST-A43
c	14	100.6	9.3	743	9	CC672052	CC672052 OGUEY84TH
	15	99.6	9.2	614	7	CF944131	CF944131 TrEST-A42
	16	99.6	9.2	737	7	CF869634	CF869634 tric019xp
	17	99.6	9.2	747	7	CF877651	CF877651 tric076xl
	18	99.6	9.2	754	7	CF877603	CF877603 tric076xf
	19	99.6	9.2	793	6	CB899781	CB899781 tric019xp
	20	99.6	9.2	803	6	CB905880	CB905880 tric076xl
	21	99.6	9.2	810	6	CB905819	CB905819 tric076xf
	22	99.4	9.2	577	6	CD874512	CD874512 AZO3.102F
	23	98	9.1	648	6	CB307629	CB307629 HFIG614_H
	24	97.6	9.1	519	7	CO750847	CO750847 EST03_A05
	25	97	9.0	776	9	CL187144	CL187144 104_402_1
	26	96.4	9.0	526	7	CV061040	CV061040 BNEL64c4
	27	96.4	9.0	550	5	BU977672	BU977672 HA11N11r
	28	96.4	9.0	559	4	BJ448151	BJ448151 BJ448151
	29	96.4	9.0	592	4	BJ481919	BJ481919 BJ481919
	30	96.4	9.0	592	7	CV061475	CV061475 BNEL69c8
	31	96.4	9.0	789	2	BF621168	BF621168 HVSMEa000
	32	96.4	9.0	850	4	BM816152	BM816152 HC111F12
	33	96.4	9.0	885	4	BM816153	BM816153 HC108B10_
	34	96	8.9	626	7	CV061550	CV061550 BNEL6C10
	35	96	8.9	751	7	CV064038	CV064038 BNEL95E6
	36	95.4	8.9	688	6	CD231034	CD231034 SS1_7_G12
	37	95.4	8.9	800	7	CN138596	CN138596 OX1_64_F0
c	38	95	8.8	826	9	CG438073	CG438073 OGVGV46TV
	39	93.8	8.7	852	7	CN145070	CN145070 WOUND1_26
	40	92.2	8.6	763	6	CB903019	CB903019 tric032xj
	41	92.2	8.6	763	7	CF872996	CF872996 tric032xj
c	42	92.2	8.6	1165	7	CK211148	CK211148 FGAS02298
	43	92	8.5	655	6	CD903989	CD903989 G356.112B
	44	91.6	8.5	1084	7	CK210592	CK210592 FGAS02241
	45	91.6	8.5	1856	3	AY104050	AY104050 Zea mays

ALIGNMENTS

```
RESULT 1
CF840561
LOCUS       CF840561          664 bp    mRNA    linear   EST 30-OCT-2003
DEFINITION  psHB009xD12f USDA-IFAFS:Expression of Phytophthora sojae genes
            during infection and propagation_sHB Phytophthora sojae cDNA clone
            sHB009D12 5, mRNA sequence.
ACCESSION   CF840561
VERSION     CF840561.1  GI:38055215
KEYWORDS    EST.
SOURCE      Phytophthora sojae
ORGANISM    Phytophthora sojae
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1  (bases 1 to 664)
AUTHORS     Tyler,B.
TITLE       Tyler,B. Not Published
JOURNAL     Unpublished (2003)
COMMENT     Contact: Tyler B
            Tyler lab
            VBI
            1880 Pratt Dr., Blacksburg, VA 24061, USA
            Tel: 540-231-7318
            Email: bmtyler@vt.edu
            PCR PRimers
            FORWARD: BK reverse primer
            BACKWARD: BK reverse primer
            Plate: 009  row: D  column: 12
            Seq primer: BK reverse primer
            High quality sequence stop: 664.
FEATURES             Location/Qualifiers
     source          1..664
                     /organism="Phytophthora sojae"
                     /mol_type="mRNA"
                     /db_xref="taxon:67593"
                     /clone="sHB009D12"
                     /tissue_type="mycelium"
                     /cell_line="P649"
                     /dev_stage="48 hr. post infection stage"
                     /lab_host="Soybean plant"
                     /clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
                     genes during infection and propagation_sHB"
                     /note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: XhoI"
ORIGIN

Query Match             33.2%;  Score 357.4;  DB 7;  Length 664;
Best Local Similarity   71.6%;  Pred. No. 1e-72;
Matches  469;  Conservative    0;  Mismatches 186;  Indels    0;  Gaps    0;
```

```
Qy  259 GTCGGCCAGACTGCGGCCACTCGGCCTTCTCGGCCGCTACCACAGCGTCAACTTTATCATC  318
            ||||| ||| || ||||| |||||||||| |||||||||||  ||| ||||| ||||
Db   10 GTGGGCCATGACGCGCCCACGGCGCGCCCTTCTCGCGCCTACCACCTGCTCAACTTCGTGATC   69

Qy  319 GGCTGCATCATGCACTCTGCGGATTTGACCGCGTTGACCGCTGGCGGCGTGACGCACCGC  378
            ||| || |||||||| |||  ||| |||||| |||  || ||||| ||||  ||||||||
Db   70 GGCACCTTCATCCACTCGCTCATCCTGAGCGCCCTTGAGTCGTGGAAGCTCACGCACCGC  129

Qy  379 CACCACCAAGAGAACACGGGCAACATTGATAAGGACGAGATCTTTTACCCGCACCGGTCG  438
            |||||||||| |||||||||||||| || |  |  |||||||| |||||||||  |||
Db  130 CACCACCAAGAACACGGGCAACATCGACGACCGGACGAGATCTTCTACCCGCAGGGCAAG  189

Qy  439 GTCAAGGACCTCCAGGACGTGGCGCCAATGGGTCTCACACGGCTCGGCGGCGTGCGTGTTTGTC  498
             || |||||| |  ||||| |  ||  | |  | ||| | ||||| |||| |||| |  ||||
Db  190 GCCGACGACCACCCCGCTCTCGCGTAACCTCATCCTGCGCGGCGCCGCGTGGTTCGCC  249

Qy  499 TACTTGAAGGTCGGGTATGCCCGCGCACGATGAGCCACTTGACCGGTGGGACCCGCTC  558
            ||| ||  |||  || | |||| |||||  ||| |||||| | ||  |||  | ||||
Db  250 TACCTGGTGCGAGGGCTTCCGCGGCGCCAAGGTCAACCACTTCAACCACCGGTTCGAGCCGCGCTG  309

Qy  559 CTCCTTCGCGCCGCGCCGTCATCGTGCTCGGCCGTCGGCCGCCGCCTTCTTCGCG  618
            || ||| |||  | |  || || | ||| || || ||||| || || |||| ||
Db  310 TTGTCCGCCAGGTGTCCGCCGTGGTCATCTCGCGGCCGCCACTTCGGCCGGTGGCCGCG  369

Qy  619 GCGTACGGCTACCTCACATACTCGCTCGGCTTTGCCGTCATGGGCCTCTACTACTATGCG  678
            | || ||||| || ||||| ||||| |||||| || | |||  | | |||||||| |||
Db  370 CTGTCCATCTACCTGAGCCTGCAGTTCGGCTTCAAGACCATGGTCATCTACTACTACGGGC  429

Qy  679 CGGCTCTTTGTCTTTGCTTCGTCGTCATTACGGACCTTCTCGTCACCACCAACGACGAA  738
            | || | | ||| | || | || | ||| |  || ||| | || |||||||||||||
Db  430 CCCGTGTTCGTGTTCGGCAGCATGCTGGTCATCCTGCGTCGTGATCATCACCACCAACGACGAGG  489

Qy  739 GCGACGCCGTGTACGGCGACTCGGAGTGGACGTACGTCAAGGGCAACCTCTCGAGCGTC  798
            | |||| || ||| |||| |||||||||| ||| ||||| ||||||||||| || ||
Db  490 GAGACCCCCGGTACGCCGGACTCGGAGTGGACTTACGTCAAGGGCAACCTCTCGTCGGTC  549

Qy  799 GACCGGCTCGTACGGCGGCGGTTCGTGGACAACCTGAGCCACGCACCAGGTC  858
            ||||| | ||||||||||| | | | | ||||| | ||| || ||||| | |
Db  550 GACCGGTCCTACGGCGGCGGCGCTCATCGACAACATCGGCACACATCGGCCGCACCAGATCC  609

Qy  859 CACCACTTGTTCCCGATCATTCCGCACTACAAGCTCAACGAAGCACCAAGCACT  913
            |||||| | ||||| ||||| |||||||| ||||||| ||  | || || |
Db  610 CACCACCTCTTCCCCATCATCCCGCACTATAAGCTCAAGCGCGGCCGCCACCGAGGGCCT  664
```

RESULT 2
CF850773/c
LOCUS   CF850773   597 bp   mRNA   linear   EST 30-OCT-2003
DEFINITION psMA015xP05f USDA-IFAFS:Expression of Phytophthora sojae genes
            during infection and propagation_sMA Phytophthora sojae cDNA clone
            sMA015P05 5, mRNA sequence.
ACCESSION   CF850773
VERSION   CF850773.1 GI:38066427
KEYWORDS   EST.
SOURCE   Phytophthora sojae
ORGANISM   Phytophthora sojae
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1 (bases 1 to 597)
AUTHORS   Tyler,B.
TITLE   Tyler,B. Not Published
JOURNAL   Unpublished (2003)
COMMENT   Contact: Tyler B
            VBI
            1880 Pratt Dr., Blacksburg, VA 24061, USA
            Tel: 540-231-7318
            Email: bmtyler@vt.edu
            PCR PRimers
            FORWARD: BK reverse primer
            BACKWARD: BK reverse Primer
            Plate: 015 row: P column: 05

Seq primer: BK reverse primer
High quality sequence stop: 597.

FEATURES   Location/Qualifiers
     source   1..597
                     /organism="Phytophthora sojae"
                     /mol_type="mRNA"
                     /db_xref="taxon:67593"
                     /clone="sMA015P05"
                     /tissue_type="mycelium"
                     /cell_line="P6497"
                     /dev_stage="mycelium"
                     /lab_host="synthetic medium"
                     /clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
                     genes during infection and propagation sMA"
                     /note="Vector: pBK-CMV; Site_1: EcoRl; Site_2: XhoI"

ORIGIN

Query Match   25.3%;   Score 273; DB 7; Length 597;
Best Local Similarity   71.3%;   Pred. No. 4.8e-53;
Matches 360; Conservative   0; Mismatches 145; Indels   0; Gaps   0;

```
Qy  560 TCCTTCGCGCCGCGTCGGCCGTCATCGTGCTCGGCCGCCGCCTTCTTCGGCCG  619
            || ||| ||||  |||  || || | ||| || || || || |||| |||
Db  594 TCGTCCGCCAGTGTCCGCCGTGGTCATCTCGCGGCCGCCACTTCGGCCGGTGGCCGGGC  535

Qy  620 CGTACGGCTACCTCACATACTCGCTCGGCTTTGCCGTCATGGGCCTCTACTACTATGCGC  679
            |||| || ||| || ||| ||| | |||||| || | |||  | | |||||||| |||
Db  534 TGTCCATCTACCTGAGCCTGCAGTTCGGCTTCAAGACCATGGTCATCTACTACTACGGGC  475

Qy  680 CGCTCTTTGTCTTTGTTGTTCCTGTCGTCATTACGGACCTTCTTCGTCACCACCAACGACGAAG  739
            | || | | |||| | | || |||| | ||| |  || ||| | || |||||||||||||
Db  474 CCGTGTTCGTGTTCGGCAGCATGCTGGTCATCCTGCGTCGTGATCATCACCACCAACGACGAGG  415

Qy  740 CGACGCCGTGGTACGGCGACTCGGAGTGGACGTACGTCAAGGGCAACCTCTCGAGCGTCG  799
            | ||| || || || |||| ||||||||| ||| ||||| ||||||||||| || ||
Db  414 AGACCCCCGGTACGCCGGACTCGGAGTGGACTTACGTCAAGGGCAACCTCTCGTCGGTCG  355

Qy  800 ACCGGCTCGTACGGCGGCGGTTCGTGGACAACCTGAGCCACGCACCACCAGGTCC  859
            ||||| | ||||||||||| | | | | ||||| | ||| || ||||||| | |
Db  354 ACCGGTCCTACGGCGGCGGCGCTCATCGACAACATCGGCACACATCGGCCGCACCAGATCC  295

Qy  860 ACCACTTGTTCCCGATCATTCCGCACTACAAGCTCAACGAAGCACCACCAAGCACTTTGCGG  919
            |||| | ||||| ||||| |||||||| ||||||| ||  | ||||| | || ||  |
Db  294 ACCACCTCTTCCCCATCATCCCGCACTATAAGCTCAAGCGCGGCCGCCACCGAGGGCCTTCCACC  235

Qy  920 CCGCGTACCGCACCTCGTGCCAGGAGACGACGAGCCATCACGGCCTTCTTCAAGA  979
            || || ||| || || | || |  ||  | || ||| || | ||| ||| |  |
Db  234 AGGCGTTCCCCGAGCTCGTGCCGAAGAGCCAAGAGCGACGACGAGCCCATCATTAAGGCCTTCTTCCCGCG  175

Qy  980 CCGCGCACCTCTTTGTCAACTACGGCCGCAGATCTTCACGCTCA 1039
            || |||| | || | ||| ||||| || |   || |||| |||
Db  174 TCGGCCGCTCTACGCCGACAACTACGGCGTCGGTGACTCGGACGACTCTTCACGCTCA  115

Qy 1040 AAGAGTCGGCGCCGGCCGCCAAGGC 1064
            ||||||| | |   |||||| |||
Db  114 AGGAGGGCCAAGGCCGTGTCCGAGGC   90
```

RESULT 3
BE777235
LOCUS   BE777235   643 bp   mRNA   linear   EST 20-SEP-2000
DEFINITION MY-26-A-10 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
ACCESSION   BE777235
VERSION   BE777235.1 GI:10230890
KEYWORDS   EST.
SOURCE   Phytophthora infestans (potato late blight agent)
ORGANISM   Phytophthora infestans
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1 (bases 1 to 643)
AUTHORS   Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
TITLE   Initial assessment of gene diversity for the oomycete pathogen
            Phytophthora infestans based on expressed sequences

```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search; using sw model

Run on:      October 11, 2005, 06:24:22 ; Search time 675 Seconds
                                          (without alignments)
                              9445.276 Million cell updates/sec

Title:       US-10-060-793A-25
Perfect score: 1077
Sequence:    1 atgactgaggataagacgaa.........ccaaggccaagtcggactaa 1077

Scoring table: IDENTITY.NUC
               Gapop 10.0 , Gapext 1.0

Searched:    4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:        8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_16Dec04:*
         1: geneseqn1980s:*
         2: geneseqn1990s:*
         3: geneseqn2000s:*
         4: geneseqn2001as:*
         5: geneseqn2001bs:*
         6: geneseqn2002as:*
         7: geneseqn2002bs:*
         8: geneseqn2003as:*
         9: geneseqn2003bs:*
        10: geneseqn2003cs:*
        11: geneseqn2003ds:*
        12: geneseqn2004as:*
        13: geneseqn2004bs:*
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1077	100.0	1077	10	AAD58792	Aad58792 Saprolegi
2	1077	100.0	1077	13	ADR20168	Adr20168 Saprolegn
3	158.6	14.7	1263	8	AAD50973	Aad50973 Caenorhab
4	157	14.6	2090	4	AAH45810	Aah45810 Chlorella
5	113.2	10.5	1543	12	ADO44397	Ado44397 Z. mays F
6	113	10.5	1089	8	ADA70102	Ado70102 Rice gene
7	107.2	10.0	1549	4	AAC82092	Aac82092 E. guinee
8	107	9.9	1182	10	AAD58806	Aad58806 Saprolegi
9	105.8	9.8	662	4	AAH45817	Aah45817 Chlorella
10	102.2	9.5	1242	10	AAD57627	Aad57627 Rice abio
11	101.6	9.4	1804	12	ADO44396	Ado44396 Z. mays F
12	100	9.3	1733	3	AAZ35178	Aaz35178 Corn delt
13	100	9.3	1733	10	AAD64462	Aad64462 Corn delt
14	97.6	9.1	1080	13	ADS48002	Ads48002 Bacterial
15	97.6	9.1	2001	12	ADM47683	Adm47683 Polynucle
16	91.6	8.5	1146	3	AAZ35183	Aaz35183 Corn delt
17	91.6	8.5	1146	10	AAD64516	Aad64516 Corn delt
18	91.6	8.5	1729	12	ADO44395	Ado44395 Z. mays F
19	91.6	8.5	1768	6	ABL58602	Abl58602 Corn micr
20	91.6	8.5	1790	2	AAQ66071	Aaq66071 Sequence
21	91.6	8.5	1790	3	AA235181	Aaz35181 Corn delt
22	91.6	8.5	1790	10	AAD64461	Aad64461 Corn delt
23	91.6	8.5	6337	3	AAZ35182	Aaz35182 Corn delt
24	90.8	8.4	6337	10	AAD64515	Aad64515 Plasmid p
25	88.4	8.2	1245	8	ADA71116	Ada71116 Rice gene
26	88.4	8.2	1308	3	AAZ51592	Aaz51592 M. charan
27	86	8.0	774	12	ADO44398	Ado44398 Z. mays F
28	83.6	7.8	1290	12	ADF89957	Adf89957 N. crassa
29	83.6	7.8	1290	12	ADF89917	Adf89917 N. crassa
30	83.6	7.8	2125	12	ADF89916	Adf89916 N. crassa
31	82	7.6	1200	3	AAZ47130	Aaz47130 Fungal de
32	82	7.6	1200	5	AAF25235	Aaf25235 Nucleotid
33	82	7.6	1200	12	ADF89956	Adf89956 M. alpina
34	82	7.6	1488	2	AAV63625	Aav63625 cDNA enco
35	82	7.6	1488	2	AAX00890	Aax00890 Mortierel
36	82	7.6	1488	2	AAQ09431	Aaq09431 M. alpina
37	81.2	7.5	546	10	ADK54845	Adk54845 Plant DNA
38	81.2	7.5	1209	8	ADA70860	Ada70860 Rice gene
39	80.6	7.5	1293	13	ADS49019	Ads49019 Bacterial
40	76	7.1	1155	12	ADM37027	Adm37027 B. juncea
41	75.8	7.0	1456	3	AAZ51591	Aaz51591 I. balsam
42	75.8	7.0	1475	9	AAD54575	Aad54575 Flax omeg
43	74.6	6.9	1398	10	ADE40488	Ade40488 P. granat
44	74.4	6.9	1206	12	ADF89919	Adf89919 A. nidula
45	74.4	6.9	1239	13	ADS49128	Ads49128 Bacterial

ALIGNMENTS

```
RESULT 1
AAD58792
ID   AAD58792 standard; DNA; 1077 BP.
XX
AC   AAD58792;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Saprolegina diclina omega-3 desaturase gene.
XX
KW   Polyunsaturated fatty acid; PUFA; omega-3 desaturase; AIDS; cosmetic;
KW   delta-12 desaturase; acquired immune deficiency syndrome; gene therapy;
KW   inflammatory skin disorder; delta-17 desaturase; eczema; animal feed;
KW   multiple sclerosis; enzyme; gene; ds.
XX
OS   Saprolegina diclina.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1077
FT                   /*tag= a
FT                   /product= "Saprolegina diclina omega-3 desaturase"
XX
PN   WO2003064596-A2.
XX
PD   07-AUG-2003.
XX
PF   21-JAN-2003; 2003WO-US001698.
XX
PR   30-JAN-2002; 2002US-00060793.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Mukerji P, Pereira SL, Huang Y;
XX
DR   WPI; 2003-689526/65.
DR   P-PSDB; AAE38732.
XX
PT   New isolated nucleic acid sequence encoding a polypeptide having
PT   desaturase activity, useful for preventing or treating eczema,
PT   burned or dry skin, AIDS, multiple sclerosis, or inflammatory skin
PT   disorders.
XX
PS   Claim 2; Fig 9B; 137pp; English.
```

```
Qy    781  GGCAACCTCTCGAGCGTCGACCGCTCGTACGGCGCGGTTCGTCTGGACAACCTGAGCCACCAC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGCAACCTCTCGAGCGTCGACCGCTCGTACGGCGCGGTTCGTCTGGACAACCTGAGCCACCAC  840

Qy    841  ATTGGCACGCACCAGGTTCCACCACTTGTTCCCGATCATTCCGCACTACAAGTCAACGAA  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ATTGGCACGCACCAGGTTCCACCACTTGTTCCCGATCATTCCGCACTACAAGTCAACGAA  900

Qy    901  GCCACCAAGCACTTTGGGCCCGCCACCTCCTGCCGAGGAACGAGCGAGCCCATC  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  GCCACCAAGCACTTTGGGCCCGCCACCTCCTGCCGAGGAACGAGCGAGCCCATC  960

Qy    961  ATCACGGCCTTCTTCAAGACCCGCCACCTCTTTGTCAACTACGGCGTGTCCCGAGACG  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  ATCACGGCCTTCTTCAAGACCCGCCACCTCTTTGTCAACTACGGCGTGTCCCGAGACG  1020

Qy   1021  GCGCAGATCTTCACGCTCAAAGAGTCGGCCGCGGCCCGCCAAGCCAAGTCGGACTAA  1077
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GCGCAGATCTTCACGCTCAAAGAGTCGGCCGCGGCCCGCCAAGCCAAGTCGGACTAA  1077
```

```
RESULT 2
ADR20168
ID   ADR20168 standard; cDNA; 1077 BP.
XX
AC   ADR20168;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Saprolegnia diclina delta-17 desaturase encoding cDNA SEQ ID NO:41.
XX
KW   oilseed plant; mature seed; seed fatty acid profile;
KW   polyunsaturated fatty acid; delta-17 desaturase; oil; food; food product;
KW   beverage; infant formula; nutritional supplement; pet food; animal feed;
KW   whole bean soy product; aquaculture food product; enzyme; gene; ss.
XX
OS   Saprolegnia diclina.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1077
FT                   /*tag= a
FT                   /*product= "delta-17 desaturase"
XX
PN   WO2004071467-A2.
XX
PD   26-AUG-2004.
XX
PF   12-FEB-2004; 2004WO-US005758.
XX
PR   12-FEB-2003; 2003US-0446941P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Kinney AJ, Cahoon EB, Damude HG, Hitz WD, Kolar CW, Liu Z;
XX
DR   WPI; 2004-625770/60.
DR   P-PSDB; ADR20169.
XX
PT   Novel oilseed plant useful for mature seeds in which total seed fatty
PT   acid profile comprises high polyunsaturated fatty acid.
XX
PS   Example 3; SEQ ID NO 41; 132pp; English.
XX
CC   The present invention describes an oilseed plant (I) that produces mature
CC   seeds in which the total seed fatty acid profile comprises at least 1.0%,
CC   5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60% or more of at least one
CC   polyunsaturated fatty acid having 20 or more carbon atoms and 5 or more
CC   carbon-carbon double bonds, and ratio of docosahexaenoic
CC   acid:eicosapentaenoic acid (DHA:EPA) is 1:100-860:100 or 1:100-110:100,
CC   where total seed fatty acid profile further comprises less than 2%
CC   arachidonic acid. Also described: (i) seeds (II) obtained from (I); (2)
CC   oil (III) obtained from (II); (3) a recombinant construct (IV) for
CC   altering the total fatty acid profile of mature seeds of an oilseed
```

```
XX
CC   The invention is directed to the identification and isolation of novel
CC   genes that encode enzymes involved in the synthesis of polyunsaturated
CC   fatty acids (PUFAs). In particular the invention is directed to genes
CC   derived from the fungus Saprolegnia diclina that encode omega-3
CC   desaturase (also referred to as delta-17 desaturase) and delta-12
CC   desaturase. Polynucleotides, composition and methods of the invention are
CC   useful for preventing or treating conditions caused by insufficient
CC   intake of at least one PUFA e.g. eczema, burned or dry skin, acquired
CC   immune deficiency syndrome (AIDS), multiple sclerosis or inflammatory
CC   skin disorders. Products produced in the method of the invention are
CC   useful in pharmaceutical and nutritional compositions, animal feeds and
CC   cosmetics. The invention is also useful in gene therapy. The present
CC   sequence is Saprolegnia diclina omega-3 desaturase gene
XX
SQ   Sequence 1077 BP; 191 A; 379 C; 286 G; 221 T; 0 U; 0 Other;

Query Match          100.0%;  Score 1077; DB 10;  Length 1077;
Best Local Similarity 100.0%; Pred. No. 6.2e-219;
Matches 1077;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1  ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGACCGCTCACGGAGCTCAAGCACTCGATC  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGACCGCTCACGGAGCTCAAGCACTCGATC  60

Qy     61  CCGAACGCGTGCTTTGAGTCGAACCTCGGCGCCTCTCGCTCTACTACACGGCCCGGCGGATC  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CCGAACGCGTGCTTTGAGTCGAACCTCGGCGCCTCTCGCTCTACTACACGGCCCGGCGGATC  120

Qy    121  TTCAACGCGTCGGCCTCGGCGGCGCGTCGCTCTACGGCGGCGGCGCCTTCGACGCCGTTCATTGCC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  TTCAACGCGTCGGCCTCGGCGGCGCGTCGCTCTACGGCGGCGGCGCCTTCGACGCCGTTCATTGCC  180

Qy    181  GATAACGTTCTGCTCCACGCGCTCGTTGCGCCACTACATCTACGTGCAGGGCGTCATC  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GATAACGTTCTGCTCCACGCGCTCGTTGCGCCACTACATCTACGTGCAGGGCGTCATC  240

Qy    241  TTCTGGGGCCTTCTTCACGGTCGGCCACGACTGCGGCCACTCGGCCTTCTCGCGCTACCAC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TTCTGGGGCCTTCTTCACGGTCGGCCACGACTGCGGCCACTCGGCCTTCTCGCGCTACCAC  300

Qy    301  AGCGGTCAACTTATCATCGGCTGCATCATGACCTCTGCGATTTTGCCGTTCGAGAGC  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AGCGGTCAACTTATCATCGGCTGCATCATGACCTCTGCGATTTTGCCGTTCGAGAGC  360

Qy    361  TGGCGCGGTGACGCACCGCCACCGCCACCGCCAAGAACACGGGCAACATTGATAAGGACGAGATC  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TGGCGCGGTGACGCACCGCCACCGCCACCGCCAAGAACACGGGCAACATTGATAAGGACGAGATC  420

Qy    421  TTTTACCCGCACCGGTCGGTCAAGGACCTCCAGGAGCGTGCGCCAATGGGTCTACACGCTC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TTTTACCCGCACCGGTCGGTCAAGGACCTCCAGGAGCGTGCGCCAATGGGTCTACACGCTC  480

Qy    481  GGCGGTGCGTGGTTTGTTCTACTTGAAGGTCGGGTATGCCCCGCGCACGATGAGCCACTTT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  GGCGGTGCGTGGTTTGTTCTACTTGAAGGTCGGGTATGCCCCGCGCACGATGAGCCACTTT  540

Qy    541  GACCCGTGGGACCCGCTCTCCTTCCGCGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GACCCGTGGGACCCGCTCTCCTTCCGCGCGTACCTCACATACTCGCTCGGCTTTGCCGTCATG  600

Qy    601  TGGGCCGCCTTCTTCGCGCGTACGGCCGCGCTACCTCCACATACTCACATTGCCGTCATG  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TGGGCCGCCTTCTTCGCGCGTACGGCCGCGCTACCTCCACATACTCACATTGCCGTCATG  660

Qy    661  GCGCTCTACTACTATGCGCCGCCTCTTCGTTGCTTCGTTCCTCGTCCATTACGACCTTC  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  GCGCTCTACTACTATGCGCCGCCTCTTCGTTGCTTCGTTCCTCGTCCATTACGACCTTC  720

Qy    721  TTGCACCAACGACGAAGCGACGACGCCGTGGTACGGACGTCGGAGTGGACGTACGTCAAG  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  TTGCACCAACGACGAAGCGACGACGCCGTGGTACGGACGTCGGAGTGGACGTACGTCAAG  780
```

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     October 11, 2005, 09:06:02 ; Search time 220 Seconds
                               (without alignments)
                               8010.318 Million cell updates/sec

Title:      US-10-060-793A-25
Perfect score: 1077
Sequence:   1 atgactgaggataagacgaa.........ccaaggccaagtcggactaa 1077

Scoring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0

Searched:   1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:       2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued_Patents_NA:*
    1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
    2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
    3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
    4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
    5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
    6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91.6	8.5	1790	3	US-09-133-962A-7	Sequence 7, Appli
2	82	7.6	1488	2	US-08-834-655-3	Sequence 3, Appli
3	82	7.6	1488	3	US-08-834-033A-3	Sequence 3, Appli
4	82	7.6	1488	3	US-09-363-574-3	Sequence 3, Appli
5	82	7.6	1488	3	US-09-363-526-3	Sequence 3, Appli
6	82	7.6	1488	3	US-09-330-235-19	Sequence 19, Appl
7	72.2	6.7	1155	3	US-08-907-608-5	Sequence 5, Appli
8	72.2	6.7	1155	3	US-09-354-231B-5	Sequence 5, Appli
9	72.2	6.7	1155	3	US-09-128-602B-5	Sequence 5, Appli
10	72.2	6.7	1155	3	US-09-482-287-5	Sequence 5, Appli
11	72.2	6.7	1155	4	US-09-966-888-5	Sequence 5, Appli
12	72.2	6.7	1155	4	US-09-995-297-5	Sequence 5, Appli
13	70.6	6.6	1155	3	US-08-907-608-3	Sequence 7, Appli
14	70.6	6.6	1155	3	US-09-354-231B-7	Sequence 7, Appli
15	70.6	6.6	1155	3	US-09-128-602B-7	Sequence 7, Appli
16	70.6	6.6	1155	3	US-09-482-287-3	Sequence 3, Appli
17	70.6	6.6	1155	4	US-09-966-888-3	Sequence 3, Appli
18	70.6	6.6	1155	4	US-09-995-297-7	Sequence 7, Appli
19	70.6	6.6	1231	1	US-08-314-596-44	Sequence 44, Appl
20	70.6	6.6	1231	3	US-08-320-982-44	Sequence 44, Appl
21	70.6	6.6	1231	3	US-08-819-037-44	Sequence 44, Appl
22	70.6	6.6	1231	3	US-09-045-940-44	Sequence 44, Appl
23	70.6	6.6	1372	3	US-09-133-962A-1	Sequence 1, Appli
24	70.6	6.6	1372	3	US-09-763-331-5	Sequence 5, Appli
25	70.6	6.6	2973	3	US-09-133-962A-15	Sequence 15, Appli
26	68.2	6.3	1155	2	US-08-675-650B-5	Sequence 5, Appli
27	67.4	6.3	1128	3	US-09-161-994A-1	Sequence 1, Appli
28	67.4	6.3	1155	2	US-08-675-650B-1	Sequence 1, Appli
29	67.4	6.3	1155	3	US-09-354-231B-9	Sequence 9, Appli
30	67.4	6.3	1155	3	US-09-354-231B-13	Sequence 13, Appli
31	67.4	6.3	1155	3	US-09-354-231B-15	Sequence 9, Appli
32	67.4	6.3	1155	3	US-09-128-602B-9	Sequence 13, Appli
33	67.4	6.3	1155	4	US-09-128-602B-13	Sequence 15, Appli
34	67.4	6.3	1155	4	US-09-128-602B-15	Sequence 13, Appli
35	67.4	6.3	1155	4	US-09-995-297-9	Sequence 15, Appli
36	67.4	6.3	1155	4	US-09-995-297-13	Sequence 3, Appli
37	67.4	6.3	1155	4	US-09-995-297-15	Sequence 1, Appli
38	67.4	6.2	1426	3	US-09-133-962A-3	Sequence 3, Appli
39	67	6.2	1155	2	US-08-675-650B-3	Sequence 11, Appli
40	65.8	6.1	1155	3	US-08-907-608-1	Sequence 17, Appli
41	65.8	6.1	1155	3	US-09-354-231B-1	Sequence 1, Appli
42	65.8	6.1	1155	3	US-09-354-231B-3	
43	65.8	6.1	1155	3	US-09-354-231B-11	
44	65.8	6.1	1155	3	US-09-354-231B-17	
45	65.8	6.1	1155	3	US-09-128-602B-1	

ALIGNMENTS

```
RESULT 1
US-09-133-962A-7
; Sequence 7, Application US/09133962A
; Patent No. 6372965
; GENERAL INFORMATION:
;  APPLICANT: JONATHAN EDWARD LIGHTNER
;             JOHN JOSEPH OKULEY
;  TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID
;                      DELTA-12 DESATURASES AND RELATED
;                      ENZYMES FROM PLANTS
;  NUMBER OF SEQUENCES: 17
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
;     STREET: 1007 MARKET STREET
;     CITY: WILMINGTON
;     STATE: DELAWARE
;     COUNTRY: UNITED STATES OF AMERICA
;     ZIP: 19898
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: DISKETTE, 3.50 INCH
;     COMPUTER: IBM PC COMPATIBLE
;     OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
;     SOFTWARE: MICROSOFT WORD VERSION 7.0A
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/133,962A
;     FILING DATE: 14-Aug-1998
;     CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: U.S. 07/977,339
;     FILING DATE: 17-NOV-1992
;  ATTORNEY/AGENT INFORMATION:
;     NAME: CHRISTENBURY, LYNNE M.
;     REGISTRATION NUMBER: 30,971
;     REFERENCE/DOCKET NUMBER: BB-1043-D
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (302)992-5481
;     TELEFAX: (302)773-0164
;     TELEX: 835420
;  INFORMATION FOR SEQ ID NO: 7:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 1790 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: double
;        TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     ORIGINAL SOURCE:
;        ORGANISM: Zea mays
;     IMMEDIATE SOURCE:
```

```
;
;   CLONE: pFad2#1
;   FEATURE:
;      NAME/KEY:            CDS
;      LOCATION:            165..1328
;   SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-133-962A-7

Query Match          8.5%;     Score 91.6;   DB 3;  Length 1790;
Best Local Similarity 47.8%;   Pred. No. 1.3e-12;
Matches 412;  Conservative  0;  Mismatches 399;  Indels 51;  Gaps  3;

Qy    96 GCTCTACTACACGGCCCGGCGATCTTCAACGCGTCGGCGGGGCGGCCTGCTCTACGC 155
         ||||| |         ||||||||||| ||||||
Db   329 GCTCAAGTCCTTCTCGTACGTGGTCCACGACCTGGTCATCGCCGGCGGCTCCTCTACTT 388

Qy   156 GGCGCCGCTCGACGCCCGTTCATTGCCGATAAACGTTCTGCTCCACGCCGTCGTTTGCGCCAC 215
         | ||| |||        ||||| ||   ||||| |
Db   389 CGCGCTGGCCATCATCACGCCGCTCCGCGCTCCCGCTACGC---CGCCTGGCCGCGCT 445

Qy   216 CTACATCTACGTGCAGGGCGTCATCTTCTGGGGCGCTTCTTCACGGTCGGCCACGACTGCGG 275
         ||        |     |||  |  | |||||
Db   446 GTACTACGTGATCGCGCAGGGGTGCGTGCACCGGCGTGTGGGTCATCGCGCACGAGTGCGG 505

Qy   276 CCACTCGGCCTTCTCGCGCTACCACCAGCGTCAAGCGGTCAACTTTATCATCGGCTTACATCG 335
         |||||||||||||| || ||||||   |||
Db   506 CCACCACGCCTTCTCGGACTACTCGCCTCTGGACGACGTGGTCGGCCTCATCGTTGCTGCACTC 565

Qy   336 TGGGATTTGACGCCGTTCGAGAGCTGGGCGTGGACGCACCGCCACCACAAGAACAC 395
         |      || ||     || ||  |   ||||||
Db   566 GTCGGCTCATGTGCCCTACTTCTCGTTGGAAGTACAGCCACCGGCGCCACCACTCCAACAC 625

Qy   396 GGGCAACATTGATAAGGACAGAGATCTTTTACCCGCCACCGGTCGGTCAAGGACCTCCAGGA 455
         ||    | |        | |||||||      ||  | |  |||||||
Db   626 GGGTCCCTGGAGCGGCGACGAGTGTTCGTGCCCAAGAGAAGGAGGGCGCTGCGCCGTGGTA 685

Qy   456 CGTGCGCCAATGGGTCTACACGCTCGGCGCGTCGTGCGGTGCGTGGTTTGTCTACTTGAA-------- 506
         |||| |         ||| ||||||||   |
Db   686 CACCCGTACGTGTACAACAACACCCGGTCGGCGGCCTGGTGCCACATCGTGGTGCAGCTCAC 745

Qy   507 ------------------------------------GGTCGGGTATGCCCCGCGCACGAT 530
                                             ||||| | |||||
Db   746 CCTCGGTGGCCGCGTGTACCTGGCCAACGCGGTCGTCTACCCGTACCCGGCCTTCGC 805

Qy   531 GAGCCACTTTGACCCGTGGACCCCGCTCCTCTTGCGCCGCGTCGGCC---GTCATCGT 587
         ||| |  ||||||||||                        |
Db   806 CTGCCCACTTCGACCCTCGACCCCTACGGCGCCCCTCACGCGGGAGCGGCCCAGATCTTCGT 865

Qy   588 GTCGGCTCGGGCGTCTGGGCCCGCGCCGTCGCCGCCTTCGCCGTACGCGTACTCACATACTCGCTCTGG 647
         |    | ||  |||||| ||       | || |||||||
Db   866 CTCGGACGCCGGCCGCGCTCGTGCGCGTGGGCGTTCGGCGCGGTCAGGGCGGTTCATTGCCGA 925

Qy   648 CTTTGCCGTCATGGGCCTCTACTACTATGCCGGCGCTCTTGTCTTTGTCTTTGCTTCGTCGT 707
         |  ||||||  ||| | ||
Db   926 CATCGATCGACTTGGGCGTCGTGCCGTTCCTGGCGTGCCACCTCTACCTGTGCCAGATCGACAAGTTTGA 985

Qy   708 GGTCGTGGTTCTTGCACCAACGACGAGCAGAGCGACGCGCCGGTACGGCGACTCGGAGTG 767
         |||||   ||  || |
Db   986 TAACGTTCTGCTCCACCTCGTTTCGCCTGGCTCGTTTACTGGATCAGGAGTATTGTCTG 1045

Qy   768 GCTCATCACCTACCTGCAGCACGCACCACCCGCCTCGCCGCTCGACGACTCGAGCGAGTG 827
         |  || |||     ||| ||||||   |||||
Db  1046 GGACTGGCTCGGCGGCGGCATCCGACTACCGCCTCCTCTCTCCACCATGCCGCGCT 1105

Qy   828 CCTGAGCGCCACCATTGGCACGCACCAGTCCACACTCTGTTCCCGATCATTCCCCACTA 887
         |||| | ||||||
Db  1106 GTTCCAACACACAGTTGGTTGGATCGTTGCACTCGATGCGTCCCCTACCACTCCTG 1165

Qy   888 CAAGCTCAACGAAGCCACCAAG 909
         |||     ||| || |||||
Db  1166 CCACGCCATGGAGGCGCCACCAAG 1187
```

```
US-08-834-655-3
;   Sequence 3, Application US/08834655
;   Patent No.5968809
;   GENERAL INFORMATION:
;      APPLICANT:   KNUTZON, DEBORAH
;      APPLICANT:   MURKERJI, PRADIP
;      APPLICANT:   HUANG, YUNG-SHENG
;      APPLICANT:   THURMOND, JENNIFER
;      APPLICANT:   CHAUDHARY, SUNITA
;      TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR SYNTHESIS
;      TITLE OF INVENTION:  OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
;      NUMBER OF SEQUENCES:  18
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
;      STREET:  260 SHERIDAN AVENUE, P.O. BOX 60039
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,655
;      FILING DATE:  11-APR-1997
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER, BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  CGNE.124.00US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 328-4400
;      TELEFAX:  (650) 328-4477
;      TELEX:  N/A
;   INFORMATION FOR SEQ ID NO: 3:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  1488 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  DNA (genomic)
US-08-834-655-3

Query Match          7.6%;     Score 82;   DB 2;  Length 1488;
Best Local Similarity 54.2%;   Pred. No. 2.5e-10;
Matches 166;  Conservative  0;  Mismatches 140;  Indels  0;  Gaps  0;

Qy   123 CAACGGCTCGGCCTCGGCGGCGGCGCTCTTCAACGCGTCTACGGCGCCGTTCATTGCCGA 182
         ||         ||||  ||||||  || |  ||||
Db   366 CATCGATCGACTTGGGCGTCGTGCCGTTCCTGGCGTGCCACCTCTACCTGTGCCAGATTTGA 425

Qy   183 TAACGTTCTGCTCCACCTCGTTTCGCCTGGCTCGTTTACTGGATCAGGAGTATTGTCTG 242
         |||| |  ||||| |  ||
Db   426 GAATCCCTGATCCGCTATTTGCCGCTGGTCGTTTACTGGATCAGGAGTATTGTCTG 485

Qy   243 CTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTCGAGCGAGTG 302
         ||       | ||||||
Db   486 CACCGGTGTCTGGGTGTGCTGGTGCTCACGAGTGTGTCATCAGTCGTTCCGCCAGAC 545

Qy   303 CGTCAACTTTATCATCGGCTTACATCGGACCCGACTCGACTCTCGCGT 362
         ||  | |||| ||
Db   546 CCTCAACAACACAGTTGGTTGGATCGTTGCACTCGATGCGTCCCTACCACTCCTG 605

Qy   363 GCGCGGTGACGACGCACGTGGCAACATTGATAAGGACACTGGGCCACCAGGTCTT 422
         |||         ||||||||
Db   606 GAGAATCTGCGACTCGAAGCACCAAGGCCACTGGCCATATGACCAAGGACCAGGTCTT 665

Qy   423 TTACCC 428
         ||
Db   666 TGTGCC 671
```

RESULT 2

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: October 11, 2005, 06:12:48 ; Search time 2675 Seconds
                                            (without alignments)
                                            933.117 Million cell updates/sec

Title: US-10-060-793A-26
Perfect score: 1929
Sequence: 1 MTEDKTKVEFPTLTELKHSI.......ETAQIFTLKESAAAAKAKSD 358

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop 6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 844130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16885260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10060793/runat_11102005_071238_6349/app_query.fasta_1.519
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10060793 @CGN_1_1_480 @runat_11102005_071238_6349
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
  1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
  2: /cgn2_6/ptodata/2/pubpna/US07_PCT_NEW_PUB.seq:*
  3: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
  4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
  5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
  6: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
  7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
  8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
  9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1929	100.0	1077	16	US-10-060-793-25	Sequence 25, Appl
2	1929	100.0	1077	19	US-10-776-311-41	Sequence 41, Appl
3	1929	100.0	1077	20	US-10-840-478-3	Sequence 3, Appli
4	1929	100.0	1077	21	US-10-840-325-35	Sequence 35, Appli
5	1929	100.0	1077	22	US-10-840-579-5	Sequence 5, Appli
6 c	1929	100.0	12456	22	US-10-985-109-95	Sequence 95, Appl
7 c	1929	100.0	12456	22	US-10-985-254-95	Sequence 95, Appl
8	1924	99.7	1077	20	US-10-840-478-62	Sequence 62, Appl
9	1924	99.7	1077	21	US-10-840-325-46	Sequence 46, Appl
10	1924	99.7	1077	22	US-10-840-579-9	Sequence 9, Appli
11	1924	99.7	10328	21	US-10-840-325-129	Sequence 129, App
12	1924	99.7	10328	22	US-10-840-579-101	Sequence 101, App
13	586.5	30.4	1080	17	US-10-369-493-26432	Sequence 26432, A
14	586.5	30.4	2001	17	US-10-310-154-101	Sequence 101, App
15	586.5	30.4	2001	21	US-10-732-923-186	Sequence 186, App
16	582	30.2	999	17	US-10-369-493-42763	Sequence 42763, A
17	572.5	29.7	1041	17	US-10-369-493-43786	Sequence 43786, A
18	529	27.4	1955	20	US-10-425-115-126240	Sequence 126240,
19	527	27.3	1666	20	US-10-425-115-126274	Sequence 126274,
20	523.5	27.1	1242	20	US-10-491-733-7	Sequence 7, Appli
21	522.5	27.1	1405	19	US-10-419-865-3	Sequence 3, Appli
22	516.5	26.8	1543	20	US-10-604-708-10	Sequence 10, Appl
23	516.5	26.8	1900	17	US-10-310-154-98	Sequence 98, Appl
24	516.5	26.8	1900	21	US-10-732-923-20	Sequence 20, Appl
25	514.5	26.7	1553	20	US-10-425-115-81874	Sequence 81874, A
26	512	26.5	1279	21	US-10-487-941-6226	Sequence 6226, Ap
27	510	26.4	1308	9	US-09-938-842A-635	Sequence 635, App
28	510	26.4	1308	11	US-09-938-842A-635	Sequence 635, App
29	510	26.4	1525	17	US-10-310-154-100	Sequence 100, App
30	510	26.4	1525	21	US-10-732-923-22	Sequence 22, Appl
31 c	509.5	26.4	1496	18	US-10-424-599-72596	Sequence 72596, A
32	508.5	26.4	1461	18	US-10-424-599-53502	Sequence 53502, A
33	506.5	26.3	1376	19	US-10-419-865-4	Sequence 4, Appli
34	506.5	26.3	1395	19	US-10-419-865-5	Sequence 5, Appli
35	506.5	26.3	1976	19	US-10-437-963-25531	Sequence 25531, A
36	505.5	26.2	1847	18	US-10-424-599-116485	Sequence 116485,
37	503.5	26.1	1350	19	US-10-776-311-47	Sequence 47, Appl
38	503	26.1	1475	16	US-10-165-289A-7	Sequence 7, Appli
39	503	26.1	2318	18	US-10-424-599-116486	Sequence 116486,
40	499.5	25.9	1662	17	US-10-310-154-99	Sequence 99, Appl
41	499.5	25.9	1662	21	US-10-732-923-21	Sequence 21, Appl
42	497	25.8	1142	16	US-10-115-571A-7	Sequence 7, Appli
43	492.5	25.5	1766	20	US-10-739-930-2687	Sequence 2687, Ap
44	492	25.5	1152	19	US-10-772-227-25	Sequence 25, Appl
45	492	25.5	1152	22	US-10-912-534-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-060-793-25
; Sequence 25, Application US/10060793
; Publication No. US2003019621A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES, ENZYMES ENCODED
; TITLE OF INVENTION: THEREBY, AND USES THEREOF
; FILE REFERENCE: 6884.US.01
; CURRENT APPLICATION NUMBER: US/10/060,793
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0

```
; SEQ ID NO 25
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-060-793-25

Alignment Scores:
Pred. No.:                1077
Score:                    1929.00
Percent Similarity:       100.00%
Best Local Similarity:    100.00%
Query Match:              Matches:        358
DB:                       Conservative:   0
                          Mismatches:     0
                          Indels:         0
                          Gaps:           16

US-10-060-793A-26 (1-358) x US-10-060-793-25 (1-1077)

Qy    1  MetThrGluAspLysThrLysValGluProThrLeuThrGluLeuLysHisSerIle  20
Db    1  ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGACCCTCACGGAGCTCAAGCACTCGATC  60

Qy   21  ProAsnAlaCysPheGluSerAsnLeuGlyLeuSerLeuTyrTyrThrAlaArgAlaIle  40
Db   61  CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCTACTACACGGCCCGCGCGATC  120

Qy   41  PheAsnAlaSerAlaSerAlaAlaLeuLeuTyrAlaAlaArgSerThrProPheIleAla  60
Db  121  TTCAACGCGTCGGCCTCGGCGGCGCTGCTCTACGCGGCGCGCTCGACGCCGTTCATTGCC  180

Qy   61  AspAsnValLeuLeuHisAlaLeuValCysAlaThrTyrIleTyrValGlnGlyValIle  80
Db  181  GATAACGTTCTGCTCCACGCGCTCGTTTGCGCCACCTACATCTACGTGCAGGGCGTCATC  240

Qy   81  PheTrpGlyPhePheThrValGlyHisHisAspCysGlyHisSerAlaPheSerArgTyrHis  100
Db  241  TTCTGGGGCTTCTTCACGGTCGGCCACCACGACTGCGGCCATTCTGGCCTTCTCGCGCTACCAC  300

Qy  101  SerValAsnPheIleIleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSer  120
Db  301  AGCGTCAACTTTATCATCGGCTGCATCATGCACTCTGCGATTTTGACGCCGTTCGAGAGC  360

Qy  121  TrpArgValThrHisArgHisHisLysAsnThrGlyAsnIleAspLysAspGluIle  140
Db  361  TGGCGGGTGACGCACCGCCACCACAAGAACACGGCAACATTGATAAGGACGAGATC  420

Qy  141  PheTyrProHisArgSerValLysAspLeuAspValArgGlnTrpValTrpTyrThrLeu  160
Db  421  TTTTACCCGCACCGGTCGGTCAAGGACCTCGACGTGCGCCAATGGGTCTACACGCTC  480

Qy  161  GlyGlyAlaTrpProValTyrLeuValGlyTyrAlaProArgMetSerHisPhe  180
Db  481  GGCGGTGCCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCGACGATGAGCCACTTT  540

Qy  181  AspProTrpAspProLeuLeuArgArgAlaSerAlaValIleValSerLeuGlyVal  200
Db  541  GACCCGTGGGACCCGCTCCTCCGCCGCGCCTCCGCCGTGATCGTGTCGCTCGGCGTC  600

Qy  201  TrpAlaAlaPheAlaAlaTyrArgLeuThrTyrSerLeuGlyPheAlaValMet  220
Db  601  TGGGCGGCCTTCGCTGCTTACCGTACGCGCTACCACATACTCGCTCGGCTTTGCCGTCATG  660

Qy  221  GlyLeuTyrTyrAlaProLeuPheValPheAlaSerPheLeuValIleThrThrPhe  240
Db  661  GGCCTCTACTACTGCCCGCTCTTTGTCTTCGTTCGTTCTCGTCATTACGACCTTC  720

Qy  241  LeuHisHisAsnAspGluAlaThrProTrpTyrGlyTrpTyrTyrValLys  260
Db  721  TTGCACCACAACGACGAAGCGACGCCGTGGTACGGCGAGTGGTACTACGTCAAG  780

Qy  261  GlyAsnLeuSerSerValAspArgSerTyrGlyAlaPheValAspAsnLeuSerHisHis  280
Db  781  GGCAACCTCTCGAGCGTCGACCGCTCGTACGGCGCGTTCGTTGGACAACCTGAGCCACCAC  840

Qy  281  IleGlyThrHisGlnValHisHisLeuHisProIleLeuProHisTyrLysLeuAsnGlu  300
Db  301  AGCGTCAACTTTATCATCGGCTGCATCATGCACTCTGCGATTTTGACGCCGTTCGAGAGC  360
```

```
Db  841  ATTGGCACGCACCAGGTTCCACCACTTGTTCCCGATCATTCGCACTACAAGCTCAACGAA  900

Qy  301  AlaThrLysHisPheAlaAlaAlaTyrProHisLeuValArgArgAsnAspGluProIle  320
Db  901  GCCACCAAGCACTTTGCGGCGGCGTACCCGCACCTCGTGCGCAGGAACGACGAGCCCATC  960

Qy  321  IleThrAlaPheLysThrAlaHisPheLeuAsnTyrGlyValAlaValProGluThr  340
Db  961  ATCACGGCCTTCTTCAAGACCGCACCACTCTTTGTCAACTACGGCGTGTGCCGAGACG  1020

Qy  341  AlaGlnIlePheThrLeuLysGluSerAlaAlaAlaAlaLysSerAsp  358
Db 1021  GCCGAGATCTTCACGCTCAAGGAGTCGGCCGCGGCCGCCAAGGCCAAGTCCGAC  1074
```

```
RESULT 2
US-10-776-311-41
; Sequence 41, Application US/10776311
; Publication No. US2004172682A1
; GENERAL INFORMATION:
;  APPLICANT: Edgar B. Cahoon
;  APPLICANT: Howard G. Damude
;  APPLICANT: William D. Hitz
;  APPLICANT: Anthony J. Kinney
;  APPLICANT: Charles W. Kolar
;  APPLICANT: Zhan Bin Liu
;  TITLE OF INVENTION: Production of Long Chain Polyunsaturated Fatty Acids in Plants
;  FILE REFERENCE: BB1538 US NA
;  CURRENT APPLICATION NUMBER: US/10/776,311
;  CURRENT FILING DATE:  2004-02-11
;  PRIOR APPLICATION NUMBER: US 60/446,941
;  PRIOR FILING DATE: 2003-02-12
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
;  LENGTH: 1077
;  TYPE: DNA
;  ORGANISM: Saprolegnia diclina
US-10-776-311-41

Alignment Scores:
Pred. No.:                5.04e-226     Length:           1077
Score:                    1929.00       Matches:          358
Percent Similarity:       100.00%       Conservative:     0
Best Local Similarity:    100.00%       Mismatches:       0
Query Match:              19            Indels:           0
DB:                                     Gaps:             0

US-10-060-793A-26 (1-358)  x  US-10-776-311-41 (1-1077)

Qy    1  MetThrGluAspLysThrLysValGluProThrLeuThrGluLeuLysHisSerIle  20
Db    1  ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGACCCTCACGGAGCTCAAGCACTCGATC  60

Qy   21  ProAsnAlaCysPheGluSerAsnLeuGlyLeuSerLeuTyrTyrThrAlaArgAlaIle  40
Db   61  CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCTACTACACGGCCCGCGCGATC  120

Qy   41  PheAsnAlaSerAlaSerAlaAlaLeuLeuTyrAlaAlaArgSerThrProPheIleAla  60
Db  121  TTCAACGCGTCGGCCTCGGCGGCGCTGCTCTACGCGGCGCGCTCGACGCCGTTCATTGCC  180

Qy   61  AspAsnValLeuLeuHisAlaLeuValCysAlaThrTyrIleTyrValGlnGlyValIle  80
Db  181  GATAACGTTCTGCTCCACGCGCTCGTTTGCGCCACCTACATCTACGTGCAGGGCGTCATC  240

Qy   81  PheTrpGlyPhePheThrValGlyHisHisAspCysGlyHisSerAlaPheSerArgTyrHis  100
Db  241  TTCTGGGGCTTCTTCACGGTCGGCCACCACGACTGCGGCCATTCTGGCCTTCTCGCGCTACCAC  300

Qy  101  SerValAsnPheIleIleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSerAla  120
Db  301  AGCGTCAACTTTATCATCGGCTGCATCATGCACTCTGCGATTTTGACGCCGTTCGAGAGC  360
```

```
                    GenCore version 5.1.6
         Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame plus_p2n model

Run on:     October 11, 2005, 06:12:42 ; Search time 5425 Seconds
                                  (without alignments)
                             3197.598 Million cell updates/sec

Title:          US-10-060-793A-26
Perfect score:  1929
Sequence:       1 MTEDKTKVEFPLTELKHSI.........ETAQIFTLKESAAAAKAKSD 358

Scoring table:  BLOSUM62
         Xgapop 10.0 , Xgapext    0.5
         Ygapop 10.0 , Ygapext    0.5
         Fgapop  6.0 , Fgapext    7.0
         Delop   6.0 , Delext     7.0

Searched:       4708233 seqs, 2422760795 residues

Total number of hits satisfying chosen parameters:     9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10060793/runat_11102005_071237_6295/app_query.fasta_1.519
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10060793 @CGN_1_1_3731 @runat_11102005_071237_6295 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :    GenEmbl:*
         1:  gb_ba:*
         2:  gb_ltg:*
         3:  gb_in:*
         4:  gb_om:*
         5:  gb_ov:*
         6:  gb_pat:*
         7:  gb_ph:*
         8:  gb_pl:*
         9:  gb_pr:*
        10:  gb_ro:*
        11:  gb_sts:*
        12:  gb_sy:*
        13:  gb_un:*
        14:  gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1929	100.0	1077	8	AY373823	Saprolegn
c 2	587.5	30.5	349050	1	AP003586	Nostoc sp
c 3	586.5	30.4	1725	1	SYCDESB	Synechocyst
c 4	586.5	30.4	143308	1	D90913	Synechocyst

```
 5  577.5  29.9     5  AJ621246    1  1762   AJ621246 Nostoc sp
 6  538.5  27.9     6  E49240      6  2090   E49240 Omega 3 fat
 7  530    27.4     7  D63353      8  1494   D63353 Zea mays FA
 8  529    27.4     8  PAB302017   8  2248   AJ302017 Picea abi
 9  528    27.3     9  AY248741    8  1308   AY248741 Lycopersi
10  527    27.3    10  SPU36389    1  2485   U36389 Synechococc
11  525    27.2    11  AY204711    8  1180   AY204711 Glycine m
12  525    27.2    12  STU007739   8  1546   AJ007739 Solanum t
13  523.5  27.1    13  AK098930    8  1612   AK098930 Oryza sat
14  523.5  27.1    14  AK061531    8  1617   AK061531 Oryza sat
15  522.5  27.1    15  AY551558    8  1320   AY551558 Malus x d
16  521    27.0    16  AB105886    8  1143   AB105886 Glycine m
17  521    27.0    17  AY157317    8  1308   AY157317 Lycopersi
18  521    27.0    18  TOBNTFAD3   8  1366   D26509 Tobacco lea
19  521    27.0    19  AR074344    6  2181   AR074344 Sequence
20  521    27.0    20  SOYCPGAD3A  8  2181   L22964 Glycine soj
21  520.5  27.0    21  AR074345    6  1675   AR074345 Sequence
22  520.5  27.0    22  SOYCPFADD   8  1675   L22965 Glycine soj
23  518    26.9    23  RCCFAD7A    8  1958   L25897 Ricinus com
24  515    26.7    24  AY135565    8  1703   AY135565 Betula pe
25  514.5  26.7    25  AB188198    8   998   AB188198 Glycine m
26  514.5  26.7    26  AY599884    8  1178   AY599884 Brassica
27  514    26.6    27  AK654569    6  1245   AK654569 Sequence
28  514    26.6    28  PCU75745    8  1556   U75745 Petroselinu
29  514    26.6    29  D79979      8  1606   D79979 Nicotiana t
30  513    26.6    30  AY135564    8  1889   AY135564 Betula pe
31  510.5  26.5    31  AY135566    8  1588   AY135566 Betula pe
32  510    26.4    32  AX505940    6  1308   AX505940 Sequence
33  510    26.4    33  AK651646    8  1308   AK651646 Sequence
34  510    26.4    34  AY078043    8  1308   AY078043 Arabidops
35  510    26.4    35  AY093304    8  1402   AY093304 Arabidops
36  510    26.4    36  ATHFAD8A    8  1525   L27158 Arabidopsis
37  510    26.4    37  AY062468    8  1605   AY062468 Arabidops
38  510    26.4    38  ATHFADIP1   8  1621   D17578 Arabidopsis
39  510    26.4    39  AF361837    8  1656   AF361837 Arabidops
40  508.5  26.4    40  AB105887    8  1131   AB105887 Glycine m
41  508.5  26.4    41  AY204712    8  1216   AY204712 Glycine m
42  508.5  26.4    42  AF020204    8  1350   AF020204 Pelargoni
43  508.5  26.4    43  AR235367    6  1353   AR235367 Sequence
44  508.5  26.4    44  BNALINDES   8  1353   L01418 Brassica na
45  508.5  26.4    45  AB051215    8  1407   AB051215 Glycine m
```

ALIGNMENTS

```
RESULT 1
AY373823
LOCUS       AY373823                1077 bp    mRNA    linear    PLN 05-MAY-2004
DEFINITION  Saprolegnia diclina omega-3 fatty acid desaturase (sdd17) mRNA,
            complete cds.
ACCESSION   AY373823
VERSION     AY373823.1  GI:38426732
KEYWORDS    .
SOURCE      Saprolegnia diclina
  ORGANISM  Saprolegnia diclina
            Eukaryota; stramenopiles; Oomycetes; Saprolegniales;
            Saprolegniaceae; Saprolegnia.
REFERENCE   1  (bases 1 to 1077)
  AUTHORS   Pereira,S.L., Huang,Y.S., Bobik,E.G., Kinney,A.J., Stecca,K.L.,
            Packer,J.C. and Mukerji,P.
  TITLE     A novel omega3-fatty acid desaturase involved in the biosynthesis
            of eicosapentaenoic acid
  JOURNAL   Biochem. J. 378 (Pt 2), 665-671 (2004)
   PUBMED   14651475
REFERENCE   2  (bases 1 to 1077)
  AUTHORS   Pereira,S.L., Mukerji,P. and Huang,Y.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-2003) 104060, Abbott Laboratories-Ross Products
            Division, RP4-3, 3300 Stelzer Road, Columbus, OH 43219, USA
FEATURES             Location/Qualifiers
     source          1..1077
                     /organism="Saprolegnia diclina"
                     /mol_type="mRNA"
```

```
601 Db  TGGGCCGCCTTCTTCGCGCGGTACGGCGTACCTCACATACTCCGCTCGGCTTTGCGGTCATG 660
221 Qy  GlyLeuTyrTyrTyrAlaProLeuPheVal PheAlaSerPheLeuVal IleThrThrPhe 240
661 Db  GGCCTCACTACTATCGCCGCTCCGCTTTGTCTTTGCTTGTCTTCCTTCGTCATTACGACCTTC 720
241 Qy  LeuHisHisAsnAspGluAlaThrProTrpTyrGlyAspSerGluTrpThrTyrValLys 260
721 Db  TTGCACCACAACGACGAAGCGACGCCGTGGTACGGCGACTCGGAGTGGACGTACGTCAAG 780
261 Qy  GlyAsnLeuSerSerValAspArgSerTyrGlyAlaPheValAspAsnLeuSerHisHis 280
781 Db  GGCAACCTCTCGAGCGTCGACCGCTCGTACGGCGCGTTCGTCGTGGACAACCTGACACCACCAC 840
281 Qy  IleGlyThrHisGlnValHisHisLeuPheProIleIleProHisTyrLysLeuAsnGlu 300
841 Db  ATTGGCACGCACCAGGTTCCACACCATCTGTTCCCGATCATTCCGCACTACAAGCTCAACGAA 900
301 Qy  AlaThrLysHisPheAlaAlaAlaTyrProHisLeuValArgArgAsnAspGluProIle 320
901 Db  GCCACCAAGCACTTGCGGCGCTACCCGCACCTCGTGCGCAGGAACGACGAGCCCATC 960
321 Qy  IleThrAlaPhePheLysThrAlaHisLeuPheValAsnTyrGlyAlaValProGluThr 340
961 Db  ATCACGGCCTTCTTCAAGACCGCCCACCTCTTTGTCAACTACGGCGTGCCCGAGACG 1020
341 Qy  AlaGlnIlePheThrLeuLysGluSerAlaAlaAlaAlaAlaLysSerAsp 358
1021 Db GCGCAGATCTTCACGCTCAAAGAGTCGGCCGCCGGCCCGGCCCAAGCCAAGTCGAC 1074
```

```
RESULT 2
AP003586/c
LOCUS       AP003586          349050 bp    DNA     linear   BCT 28-NOV-2001
DEFINITION  Nostoc sp. PCC 7120 DNA, complete genome, section 6/19.
ACCESSION   AP003586 BA000019
VERSION     AP003586.1  GI:17135283
KEYWORDS    .
SOURCE      Nostoc sp. PCC 7120
  ORGANISM  Nostoc sp. PCC 7120
            Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
REFERENCE   1
  AUTHORS   Kaneko,T., Nakamura,Y., Wolk,C.P., Kuritz,T., Sasamoto,S.,
            Watanabe,A., Iriguchi,M., Ishikawa,A., Kawashima,K., Kimura,T.,
            Kishida,Y., Kohara,M., Matsumoto,M., Matsuno,A., Muraki,A.,
            Nakazaki,N., Shimpo,S., Sugimoto,M., Takazawa,M., Yamada,M.,
            Yasuda,M. and Tabata,S.
  TITLE     Complete genomic sequence of the filamentous nitrogen-fixing
            cyanobacterium Anabaena sp. strain PCC 7120
  JOURNAL   DNA Res. 8 (5), 205-213 (2001)
  MEDLINE   21595285
   PUBMED   11759840
REFERENCE   2  (bases 1 to 349050)
  AUTHORS   Kaneko,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research
            Institute, The First Laboratory for Plant Gene Research; Yana
            1532-3, Kisarazu, Chiba 292-0812, Japan
            (E-mail:kaneko@kazusa.or.jp/cyanobase/,
            URL:http://www.kazusa.or.jp/cyanobase/,
            Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
FEATURES             Location/Qualifiers
     source          1..349050
                     /organism="Nostoc sp. PCC 7120"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:103690"
                     /note="synonym:Anabaena sp. PCC7120"
     gene            complement(572..2386)
                     /gene="all1463"
     CDS             complement(572..2386)
                     /gene="all1463"
                     /note="ORF ID:all1463
                     unknown protein"
                     /codon_start=1
```

```
                     /strain="ATCC 56831"
                     /db_xref="ATCC:56831"
     gene            1..1077
                     /gene="sdd17"
     CDS             1..1077
                     /gene="sdd17"
                     /note="SDD17; involved in desaturation of n-6 fatty acids"
                     /codon_start=1
                     /product="omega-3 fatty acid desaturase"
                     /protein_id="AAR20444.1"
                     /db_xref="GI:38426733"
                     /translation="MTEDKTKVEFPTLTELKHSIPNACFESNIGLSLYYTARAIFNAS
                     ASAALLYAARSTPFIADNVLHALVCATYIYVQGVIFWGFFTVGHDCGHSAFSRYHSV
                     NFIIGCIMHSAILTPFESWRVTHRHHHKNTGNIDKDEIFYPHRSVKDLQDVRQWVYTL
                     GGAWFVYLKVGYAPRTMSHFDPWDPLLLRRASAVIVSLGVWAAFFAAYAYLLTYSLGFA
                     VMGLYYAPLFVFASFLVITTFLHHNDEATPWYGDSEWTYVKGNLSSVDRSYGAFVDN
                     LSHHIGTHQVHHLFPIIPHYKLNEATKHFAAAYPHLVRRNDEPIITARFFKTAHLFVNY
                     GAVPETAQIFTLKESAAAAKAKSD"
ORIGIN

Alignment Scores:
Pred. No.:              Length:        1077
Score:          5.12e-183   Matches:       358
Percent Similarity:  1929.00   Conservative:    0
Best Local Similarity: 100.00%  Mismatches:      0
Query Match:         100.00%   Indels:          0
DB:                  100.00%   Gaps:            0
                          8
```

```
US-10-060-793A-26 (1-358) x AY373823 (1-1077)

  1 Qy  MetThrGluAspLysThrLysValGluPheProThrLeuThrGluLeuLysHisSerIle 20
  1 Db  ATGACTGAGGATAAGACGAAGGTCGAGTTCCCGACCCTCACGGAGCTCAAGCACTCGATC 60
 21 Qy  ProAsnAlaCysPheGluSerAsnIleGlyLeuSerLeuTyrTyrThrAlaArgAlaIle 40
 61 Db  CCGAACGCGTGCTTTGAGTCGAACATCGGCCTCTCGCTCTACTACACGGCCCGCGCGATC 120
 41 Qy  PheAsnAlaSerAlaSerAlaAlaLeuLeuTyrAlaAlaArgSerThrProPheIleAla 60
121 Db  TTCAACGCGTCGGCCTCCGGCGGCCGCTGCTCTACGGCGGCGCGCTCGACGCGCTTCATTGCC 180
 61 Qy  AspAsnValLeuLeuHisAlaLeuValCysAlaThrTyrIleTyrValGlnGlyValIle 80
181 Db  GATAACGTTCTGCTCCACGCGCTCGTTTGCGCCACCTACATCTACGTGCAGGGCGTCATC 240
 81 Qy  PheTrpGlyPhePheThrValGlyHisAspCysGlyHisSerAlaPheSerArgTyrHis 100
241 Db  TTCTGGGGCTTCTTCACGGTCGGCCACGACTGCGGCCACTCGGCCTTCTCGCGCTACCAC 300
101 Qy  SerValAsnPheIleIleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSer 120
301 Db  AGCGTCAACTTTATCATCGGCTGCATCATGCACTCACTCGGATTTTGACGCCGTTCGAGAGC 360
121 Qy  TrpArgValThrHisArgHisHisHisLysAsnThrGlyAsnIleAspLysAspGluIle 140
361 Db  TGGCGCGGTGACGCACCGGCACCACCACAAGAACACGGCAACATTGATAAGGACGAGATC 420
141 Qy  PheTyrProHisArgSerValLysAspLeuGlnAspValArgGlnTrpValTyrThrLeu 160
421 Db  TTTTACCCGCACCGGTCGGTCAAGGACCTCCAGGACGTGCGCCAATGGGTCTACACGCTC 480
161 Qy  GlyGlyAlaTrpPheValTyrLeuLysValGlyTyrAlaProArgThrMetSerHisPhe 180
481 Db  GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCGCACGATGAGCCACTTT 540
181 Qy  AspProTrpAspProLeuLeuLeuArgArgAlaSerAlaValIleValSerLeuGlyVal 200
541 Db  GACCCGTGGGACCCGCTGCTCCTCCGCCGCGCCTCGGCCGTCATCGTGTCCCTCGGCGTC 600
201 Qy  TrpAlaAlaPhePheAlaAlaTyrAlaTyrLeuThrTyrSerLeuGlyPheAlaValMet 220
```

```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    October 11, 2005, 06:12:47 ; Search time 4032 Seconds
                                       (without alignments)
                          3379.714 Million cell updates/sec

Title:          US-10-060-793A-26
Perfect score:  1929
Sequence:       1 MTEDKTKVEFPTLTELKHSI.........ETAQIFTLKESAAAAKAKSD 358

Scoring table:  BLOSUM62
          Xgapop  10.0 , Xgapext   0.5
          Ygapop  10.0 , Ygapext   0.5
          Fgapop   6.0 , Fgapext   7.0
          Delop    6.0 , Delext    7.0

Searched:       34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:      68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10060793/runat_11102005_071237_6307/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10060793 @CGN_1_1_3437 @runat_11102005_071237_6307 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY_NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     EST:*
          1: gb_est1:*
          2: gb_est2:*
          3: gb_htc:*
          4: gb_est3:*
          5: gb_est4:*
          6: gb_est5:*
          7: gb_est6:*
          8: gb_gss1:*
          9: gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description
	1	824	42.7	664	7	CF840561	CF840561 psHB009xD
	2	647	33.5	643	2	BE777235	BE777235 MY-26-A-1
c	3	595	30.8	597	2	CF850773	CF850773 psMA015xP
	4	574.5	29.8	683	7	BE776116	BE776116 MY-11-B-0
	5	529	27.4	1520	3	AY107103	AY107103 Zea mays
	6	526	27.3	1636	3	AY111307	AY111307 Zea mays
	7	503.5	26.1	1365	3	CNS0A84L	BX819659 Arabidops
	8	499	25.9	1516	3	CNS09ZRR	BX831496 Arabidops
	9	492.5	25.5	1554	3	CNS0A4NN	BX823702 Arabidops
	10	484.5	25.1	1513	3	CNS0A5G7	BX823863 Arabidops
	11	484.5	25.1	1528	3	CNS0A5PZ	BX824950 Arabidops
	12	482.5	25.0	1513	3	CNS0A5LO	BX824183 Arabidops
	13	469.5	24.3	831	7	CF215869	CF215869 CAST0002_
	14	465	24.1	1856	9	AY104050	AY104050 Zea mays
	15	460.5	23.9	833	7	CO097259	CO097259 GR__Ea21A
	16	460	23.8	869	8	CC332198	CC332198 OGIBC43TV
	17	458.5	23.8	790	7	CF443330	CF443330 EST679675
	18	458	23.7	1807	4	BI683572	BI683572 Rocheford
	19	454	23.5	737	5	BQ874237	BQ874237 QGI4M12.y
c	20	453	23.5	826	9	CG438073	CG438073 OGVGV46TV
c	21	451	23.4	900	9	CG442730	CG442730 OGVHS09TV
	22	450	23.3	724	9	BQ871133	BQ871133 QGI10P13.
	23	448.5	23.3	732	1	AJ795089	AJ795089 AJ795089
	24	441.5	22.9	757	7	CN144925	CN144925 WOUND1_25
	25	440	22.8	727	5	BU009141	BU009141 QGH9J23.y
	26	437	22.7	975	9	CG304699	CG304699 OG3B263TV
	27	436.5	22.6	707	6	CD882139	CD882139 F1.105H07
	28	435	22.6	776	9	CL187144	CL187144 104_402_1
	29	432	22.4	840	7	CO113447	CO113447 GR__Eb0I3
	30	427.5	22.2	863	7	CO082075	CO082075 GR__Ea46I
	31	426.5	22.1	824	7	CO094468	CO094468 GR__Ea16J
	32	422.5	21.9	827	7	CV290982	CV290982 aof01_3ms
	33	420	21.8	661	5	BU041344	BU041344 PP_LEA000
	34	418	21.7	1084	2	CK210592	CK210592 FGAS02241
c	35	417.5	21.6	868	7	CO199917	CO199917 GEO2_4_G0
	36	417	21.6	771	9	CC731290	CC731290 OGUB536TV
	37	414.5	21.5	763	5	BQ853589	BQ853589 QGB20018.
	38	409.5	21.2	703	5	BQ625067	BQ625067 USDA-FP_0
	39	408	21.2	701	5	BQ876051	BQ876051 QGI9N17.y
c	40	407	21.1	924	8	CC338891	CC338891 OGPBC69TV
	41	407	21.1	1065	3	CL981518	CL981518 OsIFSC045
	42	405.5	21.0	809	2	BE998745	BE998745 EST410532
	43	405.5	21.0	989	7	CK269848	CK269848 EST715926
	44	405	21.0	664	5	BQ767472	BQ767472 EBro08_SQ
	45	400	20.7	811	7	CF444900	CF444900 EST681245

ALIGNMENTS

```
RESULT 1
CF840561
LOCUS       CF840561    664 bp    mRNA    linear   EST 30-OCT-2003
DEFINITION  psHB009xD12f USDA-IFAFS:Expression of Phytophthora sojae genes
            during infection and propagation_sHB Phytophthora sojae cDNA clone
            sHB009D12_5, mRNA sequence.
ACCESSION   CF840561
VERSION     CF840561.1  GI:38056215
KEYWORDS    EST.
SOURCE      Phytophthora sojae
  ORGANISM  Phytophthora sojae
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1  (bases 1 to 664)
  AUTHORS   Tyler,B.
  TITLE     Tyler,B. Not Published
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tyler B
            Tyler lab
            VBI
            1880 Pratt Dr., Blacksburg, VA 24061, USA
            Tel: 540-231-7318
            Email: bmtyler@vt.edu
            PCR PRimers
            FORWARD: BK reverse primer
            BACKWARD: BK reverse primer
            Plate: 009  row: D  column: 12
            Seq primer: BK reverse primer
            High quality sequence stop: 664.
FEATURES             Location/Qualifiers
     source          1..664
                     /organism="Phytophthora sojae"
                     /mol_type="mRNA"
```

ORGANIZM   Phytophthora infestans
             Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
             Phytophthora.
REFERENCE   1 (bases 1 to 643)
AUTHORS   Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
TITLE   Initial assessment of gene diversity for the oomycete pathogen
             Phytophthora infestans based on expressed sequences
JOURNAL   Fungal Genet. Biol. 28 (2), 94-106 (1999)
MEDLINE   20056376
PUBMED   10587472
COMMENT   Contact: Govers F
             Laboratory of Phytopathology
             Wageningen University
             Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
             Tel: 31 317 483 138
             Fax: 31 317 483 412
             Email: Francine.Govers@medew.fyto.wau.nl.
FEATURES   Location/Qualifiers
     source   1..643
                     /organism="Phytophthora infestans"
                     /mol_type="mRNA"
                     /strain="DDR7602, A1 mating type"
                     /db_xref="taxon:4787"
                     /dev_stage="4-week old vegetative, non-sporulating
                     mycelium in synthetic medium"
                     /lab_host="E. coli, strain DH5-alpha"
                     /clone_lib="PinfestansMY"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Total
                     RNA was isolated from mycelium of P. infestans DDR7602
                     cultured for 4 weeks in synthetic medium. EST clones were
                     named by their position in the microtiter plate, preceded
                     by the prefix MY (for mycelial) and the successive number
                     of the microtiter plate (e.g. MY-06-A-04)."
ORIGIN

Alignment Scores:
Pred. No.:   Length: 643
Score: 2.25e-61   Matches: 119
Percent Similarity: 68.37%   Conservative: 28
Best Local Similarity: 55.35%   Mismatches: 64
Query Match: 33.54%   Indels: 4
DB: 2   Gaps: 2

US-10-060-793A-26 (1-358) x BB777235 (1-643)

Qy   38 ArgAlaPheAsnAlaSerAlaSerAlaAlaAlaLeuTyrAlaAlaArgSerThrPro 57
           |||| |||||| ::: ||| :::: ||| :::
Db   5 CGTTGTCTGGTGATCGCGGTGGTGCTCTAACCTGGTCCTCCAACCTCGCGCTCTGCC 64

Qy   58 PheIleAlaAspAsnValLeuLeuHisAlaLeuValCysAlaThrTyrIleTyrValGln 77
         ::: ||| ::: ||| |||| ::: |||
Db   65 GAGGTCGAGAGCTTCGTGGGCCTCTGGAGGCCGGACTGTCGCACGGGCTACATCTTCGTGCAG 124

Qy   78 GlyValIlePhePheTrpGlyPhePheThrValGlyHisAspCysGlyHisSerAlaPheSer 97
         ||| ||| ::: ||| ||| :::
Db 125 GGCATCGTGTTCTGGGGCTTCTTCACGGTGGGCCACGATCGCGGCCACCGGCGGCCTTCTCG 184

Qy   98 ArgTyrHisSerValAsnPheIleGlyCysIleMetHisSerAlaIleLeuThrPro 117
         ||| :::::   ::::::   ::::::
Db 185 CGCTACCACCTGCTAAACTTCGTGGGGTCGATCATGCACTTCATGCACCTCGCCACGCCC 244

Qy 118 PheGluSerTrpArgValThrArgHisHisHisHisLysAsnThrGlyAsnIleAspLys 137
         ::: ||||||||| ||||||
Db 245 TTCGAGTCGTGGAAGCTCACGCGTCACCACCACCACAAGAACACGGGCAACATTGACCGT 304

Qy 138 AspGluIlePheTyrProHisArgSerValLysAspLeuGlnAspValArgGlnTrpVal 157
            || ::::::::::   ::: ||| :::
Db 305 GACGAGAGTCTTCTACCCGCACCGCAAGGCCGACGACCACCCGTGTCTCGCAACCTGATT 364

Qy 158 TyrThrLeuGlyValAlaTrpPheValTyrLeuLysValGlyTyrAlaProArgThrMet 177
              |||| ::: ||| ::: |||
Db 365 CTGGCCGTCGGGGACAGCCTGGCGGTCGCCTATTTGGTCGAGGGTTCCCTCCTGTAAGTC 424

RESULT 2
BB777235
LOCUS   BB777235   643 bp   mRNA   linear   EST 20-SEP-2000
DEFINITION MY-26-A-10 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
ACCESSION   BB777235
VERSION   BB777235.1   GI:10230890
KEYWORDS   EST.
SOURCE   Phytophthora infestans (potato late blight agent)

             /db_xref="taxon:67593"
             /clone="sHB009D12"
             /tissue_type="mycelium"
             /cell_line="P6497"
             /dev_stage="48 hr. post infection stage"
             /lab_host="Soybean plant"
             /clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
             genes during infection and propagation sHB"
             /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:
Pred. No.:   Length: 664
Score: 4.29e-81   Matches: 143
Percent Similarity: 77.06%   Conservative: 25
Best Local Similarity: 65.60%   Mismatches: 50
Query Match: 42.72%   Indels: 0
DB: Gaps: 7

US-10-060-793A-26 (1-358) x CF840561 (1-664)

Qy   86 ThrValGlyHisAspCysGlyHisSerAlaPheSerArgTyrHisSerValAsnPheIle 105
         ::::|||||| ||| :::::|||||:::
Db   7 AGCGTGGGCCATGACGGCGGCCACGGCGCCCTTCTGCGCCTACCACCTGCTCAACTTCGTG 66

Qy 106 IleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSerTrpArgValThrHis 125
         ::|||| ||| |||::: ||:::
Db   67 ATCGGCCACCTTCATCCACTCCGCCATCCTGACGCCCTTCGAGTCGTGGAAGCTCACGCAC 126

Qy 126 ArgHisHisHisLysAsnThrGlyAsnIleAspLysAspGluIlePheTyrProHisArg 145
         ||||||||| |||||| ::::::::::   :::
Db 127 CGCCACCACCACAAGAACACGGGCAACATCGACCGCGACGAGATCTTCACCCCCAGCGGC 186

Qy 146 SerValLysAspLeuGlnAspValArgGlnTrpValTyrThrLeuGlyValAlaTrpPhe 165
         :::   :: ||||||| ||||||
Db 187 AAGGCCGACGACCACCCCGTCTCGCTAACCTGGGTCGTGGGCGCCGCGTGGTTC 246

Qy 166 ValTyrLeuLysValGlyTyrAlaProArgThrMetSerHisAspProTrpAspProPro 185
         ||| ::: ||| ||| :::   :::   :::
Db 247 GCCTACCTGGTCGAGGGTTCCCGCGCGCAGGTCAACCACTTCAACCCGTTCGAGCCG 306

Qy 186 LeuLeuLeuArgArgAlaSerAlaValIleValSerLeuLeuGlyValTrpAlaAlaPhePhe 205
         ||| ::::::::::||||| ::: ||||||
Db 307 CTGTTCGTCCGCCCAGTGTCGCCGGTGTCCATCTCGCTGGCCGCCGCACTTCGGCGTGGCC 366

Qy 206 AlaAlaTyrAlaTyrLeuThrTyrSerLeuGlyPheAlaValMetGlyLeuTyrTyrTyr 225
         ||| ::: |||::: ||| :::
Db 367 GCGGCGTCCATCTCACCTGAGCCTGGCAGTTCGGCTTCAAGACCATGGTCATCTACTACTAC 426

Qy 226 AlaProLeuPheValPheAlaSerPheLeuValIleThrThrPheLeuHisHisAsnAsp 245
         ||| :::   :::   ::::::   ::::::::::|||
Db 427 GGGCCCGTGTTCGTGTTCGGCAGCAGCTGTCATCACCACCTTCCTGCACCACAACGAC 486

Qy 246 GluAlaThrProTrpTyrGlyAspSerGluTrpThrTyrValLysGlyAsnLeuSerSer 265
         ||| |||||| :::|||||| |||
Db 487 GAGGAGACCCCCTGGTACGGCGACTCGGAGTGGACCTACGTCAAGGGCAACCTCTCGTCG 546

Qy 266 ValAspArgSerTyrGlyAlaPheValAlaAsnLeuSerHisHisIleGlyThrHisGln 285
         ::: ||| ::::::::: |||||| :::
Db 547 GTCGACCGCTCCTACGGCGCCTTCGTCGCCAACCTGAGCCACCACATCGGCACGCACCAG 606

Qy 286 ValHisHisLeuProIleIleProHisTyrLysLeuAsnGluAlaThrLys 303
         |||||||:::   ::::::   :::
Db 607 ATCCACCACCTCCTTCCCCATCATCCCGCACTATAAGCTCAAGGCGCCACCGAG 660

```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:     October 11, 2005, 06:12:41  ; Search time 671 Seconds
                                  (without alignments)
                         3158.372 Million cell updates/sec

Title:          US-10-060-793A-26
Perfect score:  1929
Sequence:       1 MTEDKTKVEFPTLTELKHSI........ETAQIFTLKESAAAAKAKSD 358

Scoring table:  BLOSUM62
           Xgapop  10.0 , Xgapext   0.5
           Ygapop  10.0 , Ygapext   0.5
           Fgapop   6.0 , Fgapext   7.0
           Delop    6.0 , Delext    7.0

Searched:   4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:      8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10060793/runat_11102005_071236_6287//app_query.fasta_1.519
-DB=N Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10060793 @CGN_1_1_470 @runat_11102005_071236_6287 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :   N Geneseq_16Dec04:*
           1: geneseqn1980s:*
           2: geneseqn1990s:*
           3: geneseqn2000s:*
           4: geneseqn2001as:*
           5: geneseqn2001bs:*
           6: geneseqn2002as:*
           7: geneseqn2002bs:*
           8: geneseqn2003as:*
           9: geneseqn2003bs:*
          10: geneseqn2003cs:*
          11: geneseqn2003ds:*
          12: geneseqn2004as:*
          13: geneseqn2004bs:*

                    SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1	1929	100.0	1077	10	AAD58792	Aad58792 Saprolegi
2	1929	100.0	1077	13	ADR20168	Adr20168 Saprolegn
3	586.5	30.4	1080	13	ADS48002	Ads48002 Bacterial
4	586.5	30.4	2001	12	ADM47683	Adm47683 Polynucle
5	582	30.2	999	13	ADT44325	Adt44325 Bacterial

No.	Score	%			ID	Description
6	572.5	29.7	1041	13	ADT45348	Adt45348 Bacterial
7	538.5	27.9	2090	4	AAH45810	Aah45810 Chlorella
8	523.5	27.1	1242	10	AAD57627	Aad57627 Rice abio
9	522.5	27.1	1405	12	ADJ81721	Adj81721 Mutant so
10	520.5	27.0	1675	2	AAQ43208	Aaq43208 Sequence
11	516.5	26.8	1543	12	ADO44397	Ado44397 Z. mays F
12	516.5	26.8	1900	12	ADM47680	Adm47680 Polynucle
13	514	26.6	1245	8	ADA71116	Ada71116 Rice gene
14	512	26.5	1279	10	ADK58843	Adk58843 Plant DNA
15	510	26.4	1308	8	ABZ12830	Abz12830 Arabidops
16	510	26.4	1308	8	ADA68613	Ada68613 Arabidops
17	510	26.4	1525	2	AAQ71211	Aaq71211 Linoleic-
18	510	26.4	1525	12	ADM47682	Adm47682 Polynucle
19	510	26.4	1525	13	ADS12589	Ads12589 Arabidops
20	506.5	26.3	1376	12	ADJ81722	Adj81722 Mutant so
21	506.5	26.3	1395	12	ADJ81723	Adj81723 Mutant so
22	505.5	26.2	1353	2	AAQ71203	Aaq71203 Linoleic-
23	505	26.2	2181	2	AAQ43207	Aaq43207 Sequence
24	503.5	26.1	1161	12	ADN73744	Adn73744 Thale cre
25	503.5	26.1	1268	2	AAC44312	Aac44312 Arabidops
26	503.5	26.1	1350	2	AAQ43202	Aaq43202 Sequence
27	503.5	26.1	1350	13	ADR20174	Adr20174 Arabidops
28	503.5	26.1	1350	13	ADS12587	Ads12587 Arabidops
29	503	26.1	1475	9	AAD54575	Aad54575 Flax omeg
30	500.5	25.9	1429	2	AAQ43205	Aaq43205 Sequence
31	500.5	25.9	1429	2	AAQ43206	Aaq43206 Sequence
32	499.5	25.9	1525	2	AAQ43204	Aaq43204 Sequence
33	499.5	25.9	1645	2	AAQ71210	Aaq71210 Linoleic-
34	499.5	25.9	1662	12	ADM47681	Adm47681 Polynucle
35	499.5	25.9	1662	13	ADS12585	Ads12585 Arabidops
36	499	25.9	1549	4	AAC82092	Aac82092 E. guinee
37	497	25.8	1142	3	AAS02364	Aas02364 Brassica
38	493.5	25.6	1429	3	AAC13624	Aac13624 Arabidops
39	492	25.5	1152	13	ADR87344	Adr87344 DeltaKKGG
40	492	25.5	1164	10	ABZ58386	Abz58386 Castor be
41	492	25.5	1164	13	ADR87347	Adr87347 Codon opt
42	492	25.5	1164	13	ADR87320	Adr87320 Hydroxyla
43	492	25.5	1164	13	ADR87349	Adr87349 Codon opt
44	492	25.5	1216	4	AAC89457	Aac89457 DNA found
45	489.5	25.4	1621	2	AAT62066	Aat62066 Sesame om

                              ALIGNMENTS

```
RESULT 1
AAD58792
ID   AAD58792 standard; DNA; 1077 BP.
XX
AC   AAD58792;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Saprolegina diclina omega-3 desaturase gene.
XX
KW   Polyunsaturated fatty acid; PUFA; omega-3 desaturase; AIDS; cosmetic;
KW   delta-12 desaturase; acquired immune deficiency syndrome; gene therapy;
KW   inflammatory skin disorder; delta-17 desaturase; eczema; animal feed;
KW   multiple sclerosis; enzyme; gene; ds.
XX
OS   Saprolegina diclina.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1077
FT                   /*tag= a
FT                   /product= "Saprolegina diclina omega-3 desaturase"
XX
PN   WO200306496-A2.
XX
PD   07-AUG-2003.
XX
PF   21-JAN-2003; 2003WO-US001698.
XX
PR   30-JAN-2002; 2002US-00060793.
```

```
Qy   161 GlyGlyAlaTrpPheValTyrLeuLysValGlyLeuTyrAlaProArgThrMetSerHisPhe 180
Db   481 GGCGGTGCGTGGTTTGTCTACTTGAAGGTCGGGTATGCCCCGCGCCACGATGAGCCACTTT 540

Qy   181 AspProTrpAspProLeuLeuArgArgAlaSerAlaValIleValSerLeuGlyVal 200
Db   541 GACCCGTGGGACCCGCTCCTTCGCCGGCGCCTCGGCGTCATCGTGTCGCTCGGCGTC 600

Qy   201 TrpAlaAlaPhePheAlaAlaTyrAlaTyrLeuThrThrSerLeuGlyPheAlaValMet 220
Db   601 TGGGCCGCCTTCTTCGCCGCGTACGCGTACCTCACAACTCGCTCGGCTTTGCCGTCATG 660

Qy   221 GlyLeuTyrTyrTyrAlaProLeuProPheAlaSerPheAlaLaValIleThrThrPhe 240
Db   661 GGCCTCTACTACTATGCGCCGCTCTTTGTCTTCTTGCTTCCTCGTTCCTCGTCATTACGACCTTC 720

Qy   241 LeuHisHisAspGluAlaThrProTrpTyrAspSerGluTrpTyrArgTyrValLys 260
Db   721 TTGCACCACAACGACGAGCCGACGCCGTGGTACGGCGACTCCGAGTGGTACCGCTACGTCAAG 780

Qy   261 GlyAsnLeuSerSerValAspArgSerTyrGlyAlaPheValAspAsnLeuSerHisHis 280
Db   781 GGCAACCTCTCGAGCGTCGACCGGTCGTACGGCGCGTTCGTGGACAACCTGAGCCACCAC 840

Qy   281 IleGlyThrHisGlnValHisHisLeuPheProIleLeuProHisTyrLysLeuAsnGlu 300
Db   841 ATTGGCACGCACCAGGTCCACCACTTGTTCCCGATCATTCCGCACTACAAGCTCAACGAA 900

Qy   301 AlaThrLysHisPheAlaAlaTyrProHisLeuValArgArgAsnAspGluProIle 320
Db   901 GCCACCAAGCACTTTGCGGCGTACCCGCACCTCGTGCGCAGGAACGACGAGCCCATC 960

Qy   321 IleThrAlaPhePheLysThrAlaHisLeuPheValAsnTyrGlyValProGluThr 340
Db   961 ATCACGGCCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGGCGTGCCCGAGACG 1020

Qy   341 AlaGlnIlePheThrLeuLysGluSerAlaAlaAlaAlaLysSerAsp 358
Db  1021 GCGCAGATCTTCACGCTCAAAGAGTCGGCCGCCGGCCAAGGCCAAGTCGGAC 1074
```

RESULT 2
ADR20168
ID   ADR20168 standard; cDNA; 1077 BP.
XX
AC   ADR20168;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Saprolegnia diclina delta-17 desaturase encoding cDNA SEQ ID NO:41.
XX
KW   oilseed plant; mature seed; seed fatty acid profile;
KW   polyunsaturated fatty acid; delta-17 desaturase; oil; food; food product;
KW   beverage; infant formula; nutritional supplement; pet food; animal feed;
KW   whole bean soy product; aquaculture food product; enzyme; gene; ss.
XX
OS   Saprolegnia diclina.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1077
FT   /tag= a
FT   /product= "delta-17 desaturase"
XX
PN   WO200407147-A2.
XX
PD   26-AUG-2004.
XX
PF   12-FEB-2004; 2004WO-US005758.
XX
PR   12-FEB-2003; 2003US-0446941P.
XX
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI   Kinney AJ, Cahoon EB, Damude HG, Hitz WD, Kolar CW, Liu Z;

XX
PA   (ABBO) ABBOTT LAB.
XX
PI   Mukerji P, Pereira SL, Huang Y;
XX
DR   WPI; 2003-689526/65.
DR   P-PSDB; AAE38732.
XX
PT   New isolated nucleic acid sequence encoding a polypeptide having
PT   desaturase activity, useful for preventing or treating eczema,
PT   burned or dry skin, AIDS, multiple sclerosis, or inflammatory skin
PT   disorders.
XX
PS   Claim 2; Fig 9B; 137pp; English.
XX
CC   The invention is directed to the identification and isolation of novel
CC   genes that encode enzymes involved in the synthesis of polyunsaturated
CC   fatty acids (PUFAs). In particular the invention is directed to genes
CC   derived from the fungus Saprolegina diclina that encode omega-3
CC   desaturase (also referred to as delta-17 desaturase) and delta-12
CC   desaturase. Polynucleotides, composition and methods of the invention are
CC   useful for preventing or treating conditions caused by insufficient
CC   intake of at least one PUFA e.g. eczema, burned or dry skin, acquired
CC   immune deficiency syndrome (AIDS), multiple sclerosis or inflammatory
CC   skin disorders. Products produced in the method of the invention are
CC   useful in pharmaceutical and nutritional compositions, animal feeds and
CC   cosmetics. The invention is also useful in gene therapy. The present
CC   sequence is Saprolegina diclina omega-3 desaturase gene
XX
SQ   Sequence 1077 BP; 191 A; 379 C; 286 G; 221 T; 0 U; 0 Other;

Alignment Scores:
```
Pred. No.:                  2.48e-219
Score:                      1929.00
Percent Similarity:         100.00%           Length:          1077
Best Local Similarity:      100.00%           Matches:         358
Query Match:                10                Conservative:    0
DB:                                           Mismatches:      0
                                              Indels:          0
                                              Gaps:            0
```

US-10-060-793A-26 (1-358) x AAD58792 (1-1077)

```
Qy     1 MetThrGluAspLysThrLysValGluPheProThrLeuThrGluLeuLysHisSerIle 20
Db     1 ATGACTGAGGATAAAGACGAAGGTCGAGTTCCCGACGCCTCACGGAGCTCAAGCACTCGATC 60

Qy    21 ProAsnAlaCysPheGluSerAsnLeuGlyLeuSerLeuTyrTyrThrAlaArgAlaIle 40
Db    61 CCGAACGCGTGCTTTGAGTCGAACCTCGGCCTCTCGCTCTACTACACGGCCCGCGCCGATC 120

Qy    41 PheAsnAlaSerAlaAlaAlaLeuLeuTyrAlaAlaArgSerThrProPheIleAla 60
Db   121 TTCAACGCGTCGGCCGTGCCTCGGCGCTGCTCGCCGCGCCGCGCTCCGCGTTCATTGCC 180

Qy    61 AspAsnAlaValLeuLeuHisAlaLeuValCysAlaThrTyrIleTyrValGlnGlyValIle 80
Db   181 GATAACGTTCTGCTCCACGCGCTCGTTTGCGCAACTACATCTACGTGCAGGGGCGTCATC 240

Qy    81 PheTrpGlyPhePheThrValGlyHisHisAspCysGlyHisSerAlaPheSerArgTyrHis 100
Db   241 TTCTGGGGCTTCTTCACGGTCGGCCACCGACTCGGCGCCTTCTCGCGCTACCAC 300

Qy   101 SerValAsnPheIleIleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSer 120
Db   301 AGCGTCAACTTTATCATCGGCTGCATCATGCACTCTGCGATTTTGACGCCGTTCGAGAGC 360

Qy   121 TrpArgValThrHisArgHisHisArgHisGlyAsnIleAspLysAspGluIle 140
Db   361 TGGCGCGTGACGCACCGACACCACCACACAGGGCAACATTGATAAGGACGAGAGATC 420

Qy   141 PheTyrProHisArgSerValLysAspGlnAspValArgGlnTrpValTyrArgLeu 160
Db   421 TTTTACCCGCACCGGTCGGTCAAGGACCTTCCAGGACGTGCGCCAATGGGTCTACACGCTC 480
```

```
                  GenCore version 5.1.6
         Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:   October 11, 2005, 06:12:47 ; Search time 221 Seconds
                                       (without alignments)
                                       2650.620 Million cell updates/sec

Title:         US-10-060-793A-26
Perfect score: 1929
Sequence:      1 MTEDKTKVEFPTLTELKHSI..........ETAQIFTLKESAAAAKAKSD 358

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:   2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10060793/runat_11102005_071238_6320/app_query.fasta_1.519
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10060793 @CGN_1_1_69 @runat_11102005_071238_6320 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     Issued Patents NA:*
           1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
           2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
           3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
           4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
           5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
           6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	521	27.0	2181	2	US-08-244-205-10	Sequence 10, Appl
2	521	27.0	2181	5	PCT-US92-10284-10	Sequence 10, Appl
3	520.5	27.0	1675	2	US-08-244-205-12	Sequence 12, Appl
4	520.5	27.0	1675	5	PCT-US92-10284-12	Sequence 12, Appl
5	510	26.4	1525	5	PCT-US94-01321-11	Sequence 11, Appl
6	508.5	26.4	1353	3	US-09-330-235-7	Sequence 7, Appl
7	508.5	26.4	1353	5	PCT-US94-01321-1	Sequence 1, Appl
8	503.5	26.1	1350	5	US-08-244-205-1	Sequence 1, Appl
9	503.5	26.1	1350	5	PCT-US92-10284-1	Sequence 1, Appl
10	500.5	25.9	1429	2	US-08-244-205-6	Sequence 6, Appl
11	500.5	25.9	1429	2	US-08-244-205-8	Sequence 8, Appl
12	500.5	25.9	1429	5	PCT-US92-10284-6	Sequence 6, Appl
13	500.5	25.9	1429	5	PCT-US92-10284-8	Sequence 8, Appli
14	499.5	25.9	1525	2	US-08-244-205-4	Sequence 4, Appli
15	499.5	25.9	1525	5	PCT-US92-10284-4	Sequence 4, Appli
16	499.5	25.9	1645	5	PCT-US94-01321-9	Sequence 9, Appl
17	492	25.5	1222	1	US-08-314-596-43	Sequence 43, Appl
18	492	25.5	1222	3	US-08-819-037-43	Sequence 43, Appl
19	492	25.5	1222	3	US-09-045-940-43	Sequence 43, Appl
20	492	25.5	1222	3	US-09-045-940-43	Sequence 43, Appl
21	492	25.5	1448	1	US-08-314-596-39	Sequence 39, Appl
22	492	25.5	1448	1	US-08-320-982-39	Sequence 39, Appl
23	492	25.5	1448	1	US-08-819-037-39	Sequence 39, Appl
24	492	25.5	1448	3	US-09-045-940-39	Sequence 39, Appl
25	481.5	25.0	1369	3	US-09-133-962A-11	Sequence 11, Appl
26	465	24.1	1790	3	US-09-133-962A-7	Sequence 7, Appli
27	459.5	23.8	1462	3	US-09-133-962A-5	Sequence 5, Appli
28	458	23.7	1155	3	US-08-907-608-5	Sequence 5, Appli
29	458	23.7	1155	3	US-09-354-231B-5	Sequence 7, Appli
30	458	23.7	1155	3	US-09-354-231B-7	Sequence 7, Appli
31	458	23.7	1155	3	US-09-128-602B-5	Sequence 5, Appli
32	458	23.7	1155	3	US-09-128-602B-7	Sequence 5, Appli
33	458	23.7	1155	3	US-09-482-287-5	Sequence 5, Appli
34	458	23.7	1155	4	US-09-966-888-5	Sequence 5, Appli
35	458	23.7	1155	4	US-09-995-297-5	Sequence 5, Appli
36	458	23.7	1155	3	US-09-995-297-7	Sequence 7, Appli
37	457	23.7	1155	3	US-09-354-231B-9	Sequence 9, Appli
38	457	23.7	1155	3	US-09-128-602B-9	Sequence 9, Appli
39	457	23.7	1155	4	US-09-995-297-9	Sequence 9, Appli
40	457	23.7	1426	3	US-09-133-962A-3	Sequence 3, Appli
41	455	23.6	1155	3	US-08-907-608-3	Sequence 3, Appli
42	455	23.6	1155	3	US-09-482-287-3	Sequence 3, Appli
43	455	23.6	1155	4	US-09-966-888-3	Sequence 3, Appli
44	454	23.5	1155	4	US-09-354-231B-11	Sequence 11, Appl
45	454	23.5	1155	3	US-09-128-602B-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
US-08-244-205-10
; Sequence 10, Application US/0824205
; Patent No. 5952544
; GENERAL INFORMATION:
;    APPLICANT:  Browse, John, Kinney, Anthony J.,
;    APPLICANT:  Pierce, John, Wierzbicki, Anna M.,
;    APPLICANT:  Yadav, Narendra S., Perez-Grau, Luis
;    TITLE OF INVENTION:  Fatty Acid Desaturase Genes
;    TITLE OF INVENTION:  from Plants
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  E. I. du Pont de Nemours and Company
;       STREET:  1007 Market Street
;       CITY:  Wilmington
;       STATE:  Delaware
;       COUNTRY:  U.S.A.
;       ZIP:  19898
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Macintosh
;       OPERATING SYSTEM:  Macintosh System, 6.0
;       SOFTWARE:  Microsoft Word, 4.0
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/244,205
;       FILING DATE:
;       CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/804,259
;       FILING DATE:  4 DECEMBER 1991
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  Floyd, Linda A.
;       REGISTRATION NUMBER:  33,692
;       REFERENCE/DOCKET NUMBER:  BB-1036-A
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (302) 992-4929
```

```
      TELEFAX: (302) 892-7949
      TELEX: 835420
;  INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 2181 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;    ORGANISM: Glycine max
;   IMMEDIATE SOURCE:
;    CLONE: pXF1
;   FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 855..1997
US-08-244-205-10

Alignment Scores:
Pred. No.:
Score:                    1.32e-54          Length:         2181
Percent Similarity:       521.00            Matches:        118
Best Local Similarity:    55.06%            Conservative:   56
Query Match:              37.34%            Mismatches:     118
DB:                       27.01%            Indels:         24
                                            Gaps:           10
                                                            2

US-10-060-793A-26 (1-358) x US-08-244-205-10 (1-2181)

Qy   13 LeuThrGluLeuLysHisSerIleProAsnAlaCysPheGluSerAsnGlyLeuSer     32
           :::||||||     |||||||||   |||::
Db  957 ATTGCAGAAATCAGAGCTTCAATACCAAAAACATTGCTGGGTCAAGAATCCATGGAGATCC 1016

Qy   33 LeuTyrTyrThrAlaArgAlaIlePheAsnAlaSerAlaSerAlaAlaLeuLeuTyrAla   52
           ||||   |::           |||:::
Db 1017 CTCAGTTATGTTCTCAGGGATGTGCTT------GTAATTGCTGCATTGGTGGCTGCA     1067

Qy   53 AlaArgSerThrProPheIleAlaAspAsnValLeuLeuHisAlaLeuValCysAlaThr   72
          |||          ||||||:::|||   ||||:::|||
Db 1068 GCA---------ATTCACTTCGACAACTGGCTTCTCTGGCTAATCTATTGCCCC---    1112

Qy   73 TyrIleTyrValGlnGlyValIlePheTrpGlyPhePheThrValGlyHisAspCysGly   92
              ||||||:::        |||||||:::|||:::||
Db 1113 -------ATTCAAGGCACAATGTTCTGGGCTCTCTTTGTTCTTGGACATGATTGTGGC   1163

Qy   93 HisSerAlaPheSerArgTyrHisSerValAsnPheIleIleGlyCysIleMetHisSer  112
          :::|||      :::|||||:::|||||||||
Db 1164 CATGGAAGCTTTTCAGATAGCCCTTGCTGAATAGCCTGGTGGGACACACATTGCCATTCC 1223

Qy  113 AlaIleLeuThrProPheGluSerTrpArgValThrHisHisArgHisHisLysAsnThr  132
          :::|||||:::::|||     |||||||:::||
Db 1224 TCAATTCTTGTGCCATACCATGGATGGAGAATTAGCCACAGAACTCCACCATCAAAAACCAT 1283

Qy  133 GlyAsnIleAspLysAspGluIlePheTyrPro-----HisArgSerValLysAspLeu  150
          ||||||:::||   :::|:::||
Db 1284 GGACACATTGAGAAGGAAGATGAGTCATGGGTTCATTAACAGAAGAGATTTACAAGAATCTA 1343

Qy  151 GlnAspValArgGlnTrpVal---TyrThrLeuGlyAlaTrpPheVal---------     166
          :::      ::   :::||:::||
Db 1344 GACAGCGATGACAAGACTCATTAGATTCACTGCGCCATTCCATTGTTTGTGTATCCAATT 1403

Qy  167 TyrLeuLysValGlyTyrAlaProArgThrMetSerHisPheAspTrpAspProLeu    186
          :::          |||:::
Db 1404 TATTTGTTTCAAGAAGCCCCGAAAGGAAGGCTCTCACTTCAATCCCTACAGCAATCTG   1463

Qy  187 Leu---LeuArgArgAlaSerArgAlaValIleValSerLeuGlyValTrpAlaAlaPhePhe 205
          :::     :::|||
Db 1464 TTCCCACCAGTGAGAAGAAGGAATAGCAATATCAACACTGTGTTGGGCTACCATGTTT   1523

Qy  206 AlaAlaTyrAlaTyrLeuThrTyrSerLeuGlyPheAlaValMetGlyLeuTyrTyrTyr  225
          :::|||:::::::::
Db 1524 TCTCTGCTTATCTCATTCAATAACTAGTAGTCCACTTCAGTGCTCAAGCTCTATGGA    1583
```

```
Qy  226 AlaProLeuPheValPheAlaSerPheLeuValIleThrThrPheLeuHisHis-----  243
          |||          :::||||     :::|||
Db 1584 ATTCCATATTGGATATTTGTATGTGGCTGGACTTTGTCACATACTTGCATCCATGGT    1643

Qy  244 AsnAspGluAlaThrProTyrGlyAspSerGluTrpThrTyrValLysGlyAsnLeu     263
          :::   :::|||:::
Db 1644 CACCACCAGAAACTGCCTTGGTACCGCGGCCAAGGAATGGAGTTATTTAAGAGGTGGCCTC 1703

Qy  264 SerSerValAspArgSerTyrGlyAlaPheValAspAsnLeuSerHisHisIleGlyThr  283
          :::||||||:::|||||||||
Db 1704 ACCACTGTGGATCGTGACTATGGT---TGGATCTATAACATTCACCATGACATTGGCACC 1760

Qy  284 HisGlnValHisHisLeuPheProIleIleProHisTyrLysLeuAsnGluAlaThrLys  303
          |||:::||||||       :::|||
Db 1761 CATGTTATCCACCATCTTTTCCCCAAATTCCTCATTATCATTCACCTCGTTGAAGCGACACAA 1820

Qy  304 HisPheAlaAlaTyrProHisLeuValArgArgAsnAspGluPro    319
          |||          :::
Db 1821 --------GCAGCAAAACCAGTTCTTGGAGATTACTACCGTGAGCCA   1859
```